Human L49 Human L49 Human L49 Fusion pr Mouse 14.

Human Human Human Human

Anti-huma Anti-huma Anti-huma

TSH recep

Human L49 Human L49

Adm33981 Abp96777 Abp96777 Abp96777 Abp96777 Abp9678 Abp12916 Abp12916 Abp4865 Abp4865 Abp4865 Abp4865 Abp4865 Abp4865 Abp4865 Abp4865 Abp4863 Abp4863

Anti-huma

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immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy; cancer; cell surface glycosphingolipid.
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                 ADM3381
ABP96778
ABP96778
AAY80284
AAW71879
AAW1293
AAW87293
ADP48650
ADP48
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/label= huVLFR3
/note= "framework r
104. .113
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// 13bel= huvLFR2
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WO2004055056-A1
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Synthetic.
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Region
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Adp42956 Humanised Adp42960 Humanised Adp42960 Humanised Ade77858 14.18 ant Aar11598 Murine mo Adg67526 14.18 ant Adg67526 14.18 ant Adg67514 14.18 ant Adg67514 14.18 ant Adg67514 14.18 ant Adg67514 Humanised Ady870753 Humanised Ady870938 Humanised Adg55715 Humanised Adg55716 Humanised Adg57197 Anti-huma Ada71877 Anti-huma Ada72914 Anti-huma Ada72914 Anti-huma Ada72914 Anti-huma Ada72919 Anti-huma Ada72919 Humiahuma Ada72919
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1 DVVMTQTPLSLPVTFGEPAS......SQSTHVPFLTFGAGTKLELK
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents humanised immunoglobulin light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents humanised immunoglobulin light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified m14.18 antibodies with reduced immunogenicity and that specifically bind the human cell surface glycosphingolipid GD2, useful for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                         immunoglobulin; antibody; GD2; cytostatic; gene therapy; cancer; cell surface glycosphingolipid.
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                                                                                                                                                                                                      Length 113;
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                                                                                                                                                                                                     ; Score 595; DB 8;
; Pred. No. 1.3e-43;
0; Mismatches 0;
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                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 113; Conservative
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N-PSDB; ADP42959.
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К;
                                                                                                                                                                       Sequence 113 AA,
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Length 220;

100.0%; Score 595; DB 8;

Sequence 220 AA;

Query Match

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                                                                                                                                                                                                                                                                                                                                                           Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                              1 DVVWTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New modified fusion protein with reduced immunogenicity, useful combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
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                             Indels
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              red. No. 2.4e-43;
Mismatches 0;
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Way JC;
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                                                                                                                                                                                                                                  AAE27856 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                              antibody VK region #2.
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'ਸ਼ਿਸ਼ '80.001
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Baker M,
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05-APR-2001; 2001EP-00108291.
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Best Local Similarity 96.5
Matches 109; Conservative
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Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-667054/71.
         Best Local Similarity
Matches 113; Conserv
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SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113

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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MRC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule dentified is useful for preparing a biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
                                                                                                                                                                                                        human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams S,
                                                                                                                                                                               14.18 antibody VK mouse modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 21; Page 67; 85pp; English.
                                                                                        Z
                                                                                       ADG67528 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001EP-00110220.
2001EP-00113228.
2001EP-00124965.
2001EP-00126859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones T,
                                                                                                                                                                                                                                                                                                                                                                                                                                     2001EP-00106899.
2001EP-00107012.
2001EP-00107568.
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2001EP-00106536
                                                                                                                                                                                                                                                                                                                                                                                                                       2001EP-00106538
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to MHC molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                                                                                                                                                                                                                                                    WO200269232-A2
                                                                                                                                                                                                                                                                                                                                              18-FEB-2002;
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27-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                           08-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2001;
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                                                                                                                                                                                                                                                                                                                  06-SEP-2002
                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding
                                                                                                                                                                                                                                                        Mus sp
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Two separate H and L chain cDNA libraries were prepared from mRNA isolated from the murine hybridoma cell line 14.18. The lambda gil0 library was enriched for full-length L- and H-chains. It was screened by filter hybridisation using various C region probes. Ten phage clones from each screening were analysed further by restriction analysis. The L chain cDNA sequence was sequenced and the amino acid sequence deduced from it. It appears to include a 19 amino acid leader followed by sequences that are highly homologous to the anti- GAT family of V(Kappa) genes. See also AAQ11291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein prodn. - e.g. having dual biological activity, esp. antibodies, by transfecting host cell with constructed cassette and second DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                           chimaeric binding protein; immunoglobulin; variable region; mouse;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.8%; Score 570; DB 2; Length 150; 96.5%; Pred. No. 2.3e-41; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                    Murine monoclonal 14.18 L chain V region.
                                                                                                                                                                                                                                                                                              /label= variable region
                                                                                                                                                                                                                                                                                                                                 133. .151
/label= kappa C region
                                                                                                                                                                                                                                                        l. .19
/label= leader peptide
                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         121. .132
/label= J(kappa5)
                                                                        AAR11598 standard; protein; 150
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                                                                                                                                                                                                                                                                                                                                                                                                                           89US-00409889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ11292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT
                                                                                                                          14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-1989;
                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-1991.
                                                                                                                                                                                           light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gillies SD;
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                                                                                                 AAR11598;
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Length 113; Indels

95.8%; Score 570; DB 5; L llarity 96.5%; Pred. No. 1.8e-41; Conservative 2; Mismatches 2;

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DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF

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us-10-737-208a-1.rag

AAE27854;

AAE27854 RESULT

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Mus sp.

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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MIC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
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                                                                                                          human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
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                                                                    14.18 antibody VK mouse peptide threaded modified epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 558; DB 5;
94.7%; Pred. No. 1.9e-40;
iive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 21; Page 67; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones T,
                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2001; 2001EP-00105777.
15-MAR-2001; 2001EP-00106536.
15-MAR-2001; 2001EP-00106538.
20-MAR-2001; 2001EP-00106899.
20-MAR-2001; 2001EP-00107012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2001; 2001EP-00110220.
                                                                                                                                                                                                                                                                                                             18-FEB-2002; 2002WO-EP001688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001EP-00107568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2001; 2001EP-00124965.
12-NOV-2001; 2001EP-00126859
                        11-MAR-2004 (first entry)
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Best Local Similarity 94.7³
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding to MHC molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr FJ, Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113 AA;
                                                                                                                                                                                                                       WO200269232-A2.
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                                                                                                                                                                                Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological or properties of a composition which elicits biological effects such as nauses or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                  Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
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SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter G,
Way JC;
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                                                                                                                                                                                                                                       Mouse 14.18 antibody VK region #1.
                                                                                                        AAE27854 standard; protein; 113
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Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.8%;
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                                                                                                                                                                                              (first entry)
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Best Local Similarity 94.7
Matches 107; Conservative
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Watkins J,
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Hanlon M,

Hamilton A;

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ADG67526;

RESULT 7 ADG67526

Length 113;

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AAB21363 standard; protein; 114 AA

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MHC; gastric upset; nausea; 14.18 antibody.
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                                               WO200266514-A2
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                                                                                                                                                                                                                                                                               polypeptide.
                                                                      29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                             Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal antibody having high affinity and useful for treating IL-18 mediated disorders such as multiple sclerosis, rheumatoid arthritis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the light chain variable region of the mouse antibody 1369. The antibody has high affinity for human interleukin-18 (IL-18) and is useful for treating and diagnosing IL-18-mediated disorders, e.g. autoimmune diseases such as multiple sclerosis, rheumatoid arthritis, type I or insulin dependent diabetes, inflammatory bowel disease and psoriasis. Specific changes can be introduced into the nucleotide sequences encoding the complementarity determining regions (CDRs) or framework regions of the variable light chain and heavy chain peptides. The resulting modified or fusion nucleic acid sequences can then be introduced into a plasmid for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                     antibody 13G9; antiarthritic; immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; fusion protein; immunological; major histocompatability complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGWTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                               antiinflammatory; antipsoriatic; interleukin-18; IL-18; autoimune disease; multiple sclerosis; rhematoid arthritis; type I diabetes; insulin dependent diabetes; IDDM; psoriasis; inflammatory bowel disease; complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.9%; Score 547; DB 3; Length 114; 92.0%; Pred. No. 1.7e-39; ive 4; Mismatches 5; Indels
                                              Mouse antibody 13G9 light chain variable region.
                                                                                                                                                                                                                                                                                                      Abdel-Meguid SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 14.18 antibody VK modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE27842 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 3; 64pp; English.
                                                                                                                                                                                                                                                                SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                    Taylor AH,
                                                                                                                                                                                                                  17-MAR-2000; 2000WO-US007349
                                                                                                                                                                                                                                         99US-0125299P.
                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 92.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                            WPI; 2000-628249/60.
                                                                                                                                                                                                                                                                                                      Holmes SD,
                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA99642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114 AA;
                                                                                                                                                                  WO200056771-A1.
                                                                                                                                                                                                                                         19-MAR-1999;
                                                                                                                                             musculus
                      25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2002
                                                                                                                                                                                          28-SEP-2000
AAB21363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                 (SMIK)
                                                                                                                                                                                                                                                                                                    Ho YS,
                                                                                                                                            Mus
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derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which alicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQSPGTLPVSLGERATISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                         useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to an immunogenically modified fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLTISRLEAEDLAVYFCSQSTHVPPLTFGQGTKLEIK 113
                                                                                                                                                                                                                                      Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                  New modified fusion protein with reduced immunogenicity, usefu
combining favorable properties of a composition, comprises an
immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 532; DB 5; Length 113;
Pred. No. 3.3e-38;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                      Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.18 antibody VK veneered modified epitope.
                                                                                                                                                                                                                                      ϋ
                                                                                                                                                                                                                                      Carter G,
Way JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 19; Page 77; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                      Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG67514 standard, protein; 113
                                                               19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.48;
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                                                                                                                                                                   (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 101; Conservative
                                                                                                                                                                                                                                   Gillies S, Carr FJ,
Hanlon M, Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates
                                                                                                                                                                                                                                                                                                                                      WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Gaps

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DNA encoding mutant ICAM-R poly:peptide(s) - useful for diagnosis and treatment of cell adhesion based disease conditions e.g. inflammation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Col 119-122; 111pp; English.
                                                                                                                                                                                                                                                                                                                             Vazeux R, Gallatin WM;
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-530940/45.
                                                                                                                                                                                                                                                                                          (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV54860
                                                                                                                                                                                            22-JAN-1993;
26-JAN-1993;
05-AUG-1993;
                                                                                                    07-JUN-1995;
                           US5811517-A
                                                                                                                                                                                                                                                       05-AUG-1994;
                                                                22-SEP-1998
                                                                                                                                         27-JAN-1992
                                                                                                                                                          26-MAY-1992
                                                                                                                                                                            05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma.
         The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a bological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful to preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-peptide within the amino acid sequence of a parent immunogenically non-pointed biological molecule dentified is useful for preparing a biological molecule with where the T-cell epitope desired blological activity, where the T-cell epitope is a limer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                      Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.4%; Score 532; DB 5; Length 113; 89.4%; Pred. No. 3.3e-38; Live 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                        Hamilton A;
                                                                                                                                                                                                                                                                                                    Williams S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 21; Page 66; 85pp; English.
                                                                                                                                                                                                                                                                                                    Jones T,
                                                                                      2001EP-00106538
2001EP-00106899
                                                                                                                                                   2001EP-00107568
                                                                                                                                                                                                      19-OCT-2001; 2001EP-00124965.
12-NOV-2001; 2001EP-00126859.
18-FEB-2002; 2002WO-EP001688
                                                                        2001EP-00106536
                                                                                                                                   2001EP-00107012
                                                                                                                                                                  2001EP-00110220
                                                                                                                                                                                        2001EP-00113228
                                                                                                                                                                                                                                                             (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 101; Conserval
                                                                                                                                                                                                                                                                                                    Carter G,
                                                                                                                                                                                                                                                                                                                                     WPI; 2002-750424/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 113 AA;
                                                                                                                           20-MAR-2001;
27-MAR-2001;
25-APR-2001;
                                                                                        15-MAR-2001;
20-MAR-2001;
                                                    08-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                      30-MAY-2001;
                                                                                                                                                                                                                                                                                                  Carr FJ,
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92US-00827689. 92US-00889724. 92US-00894061. 93US-0009266. 93WO-US000787.

93US-00102852 94US-00286754

95US-00483389

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The present sequence represents the humanised light chain of murine antibody (16.8.1. This antibody is specific for ICAM-R (intercellular adhesion molecule-R). ICAMs are polypeptides that are expressed on blood vessel endothelial cell surfaces and are involved in the adhesion events in various conditions. ICAM-R variants (see AAW71264-69) can be used to nonspecific immune responses, asthma, tumour growth and/or metastasis and viral infections. The ICAM variants are produced recombinantly, from varpression libraries of mutated sequences, and the ones that are claimed are the ones that have been found to be especially involved in adhesion events. They can also be used to raise antibodies, also for use as the appearance or diagnostic agents. (Updated on 25-MAR-2003 to correct PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intercellular adhesion molecule; human; ICAM-R; modulator; 14.3.3 family; HS1-beta; tubulin; inhibitor; stimulator; effector; immune response; inflammation; disorder; T cell activation; macrophage; Crohn's disease; adult respiratory distress syndrome; stroke; multiple sclerosis; asthma; rheumatoid arthritis; tumour growth; human immune deficiency virus; infection; diabetes; graft vs. host disease; passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 DIWATQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.2%; Score 530.5; DB 2; Length 116; larity 88.5%; Pred. No. 4.5e-38; Conservative 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ICR-8.1 V-K region PCR product protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW76126 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW76126;
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Gaps

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9 9

1 DVVMTQTPLSLPVTPGPPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 

Conservative

61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113 

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Human, ICAM-R, intercellular adhesion molecule; adhesion; treatment; inflammatory condition; asthma; tumour growth; metastasis; viral infection; antibody ICR-8.1.

Mús sp. Homo sapiens

Synthetic.

Humanised murine antibody ICR-8.1 light chain amino acid sequence.

(first entry)

(revised)

25-MAR-2003 18-NOV-1998

AAW71256;

AAW71256 standard; protein; 116 AA

RESULT 11 AAW71256

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The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies targeted to the human intercellular adhesion molecule polypeptide (ICAM-R) polypeptide. Antibodies specific for ICAM's are potentially useful as therapeutic compounds, for treating e.g. immune-mediated inflammatory conditions (e.g. graft-versus-host disease), asthma, tumours or viral infections. Monoclonal antibodies specific for ICAM-R, or their conjugates formed with e.g. toxins or radionuclides are useful for therapeutically targeting or detecting neovascularisation sites. The present sequence represents the amino acid sequence of the VK region of the humanised antibody ICR-8.1
monoclonal antibody; therapeutic; inflammatory; asthma; tumour; sus-host disease; viral infection; toxin; radionuclide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibodies specific for intercellular adhesion molecule polypeptide - useful for therapeutic or diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICAM-R, murine; intercellular adhesion molecule; phosphorylation; protein kinase C; modulator; ICR-8.1; VH region; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%; Score 530.5; DB 2; Length 116; 88.5%; Pred. No. 4.5e-38; ive 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanised murine antibody ICR-8.1 VK region HuVK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 13; Col 131-132; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAYS0753 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                        920S-00889724.
920S-00894061.
93US-0009266.
93WO-US000787.
93US-00102852.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 100; Conservative
                                         neovascularisation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vazeux R, Gallatin WM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-023535/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV69174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Homo sapiens.
                                                                                     Mus sp.
Homo sapiens.
                                                                                                                                                                                                                                 07-JUN-1995;
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                                                                                                                                              US5837822-A.
                                                                                                                                                                                       17-NOV-1998
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05-JUN-1992
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26-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1993
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AAY50753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human ICR-8.1 V-K region amplified PCR product. This sequence is used in the isolation of a novel human intercellular adhesion molecule, ICAM-R. This sequence is used in a method which investigates modulators of the interaction between ICAM-R and the 14.3.3 family member HS1-beta and tubulin. An anti-ICAM-R and the 14.3.3 family member HS1-beta and tubulin. An anti-ICAM-R peptide, can block, inhibit or stimulate ligand/receptor interactions involving ICAM-R, particularly its effector functions involved in involving ICAM-R, particularly its effector functions involved in treat or monitor inflammation, disorders involving T cell activation or macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth, human immune deficiency virus infection, diabetes, graft vs. host disease and many others. Antibodies may also be used for passive immunisation, for purifying, detecting or quantifying ICAM-R and for identifying ICAM-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compounds that modulate interaction of intracellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule R - with ligands HS1-beta and tubulin using two-hybrid assay, useful for treating inflammation, T cell activation etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQXPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.2%; Score 530.5; DB 2; Length 116; 88.5%; Pred. No. 4.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised antibody ICR-8.1 Vk region (HuVK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 13; Col 120-121; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW81450 standard; protein; 116 AA.
                                                                                                                                                                                   92US-00827689.
92US-00889724.
92US-00894061.
93US-00009266.
93WO-US000787.
                                                                                                                                              95US-00482882
                                                                                                                                                                                                                                                                                            93US-00102852
94US-00286754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Gallatin WM, Vazeux R;
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-386989/33.
                                                                                                                                                                                                                                                                                                                                                           CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV56402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for purifying, de
expressing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                           SODI (-SODI)
                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1999
                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                  05-AUG-1994;
                                                             US5773218-A
                                                                                                    30-JUN-1998
                                                                                                                                                                                       27-JAN-1992
                                                                                                                                                                                                           26-MAY-1992
05-JUN-1992
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Gaps

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Hybrid fusion proteins comprising intercellular adhesion molecule or its variants useful, for treating inflammatory conditions, Crohn's disease, atherosclerosis and diabetes.
                                                                                                                                                                                                                                                                                                                   Example 13; Col 121-122; 109pp;
                                                                                                                                                                                                                                        WPI; 2000-542449/49.
                                                                                                                                                                                              (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                    N-PSDB; AAA97144.
                                                                                                                                                                                                                  Gallatin WM,
                                                                                  07-JUN-1995;
                                                                                                                                        22-JAN-1993;
26-JAN-1993;
05-AUG-1993;
                                       US6100383-A.
                                                                                                                                                                         05-AUG-1994;
                                                             08-AUG-2000
                                                                                                         27-JAN-1992
                                                                                                                     26-MAY-1992
                   Synthetic.
      This invention describes a novel method for identifying a compound that modulates phosphorylation of human intercellular adhesion molecule polypeptide (IGAM-R) by protein kinase C isoform. The method comprises: (a) exposing a purified peptide consisting of the cytoplasmic domain of ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in phosphate transferred to the peptide; and (c) identifying a test compound; (b) measuring labeled that affects transfer of the labeled phosphate as a modulator compound that affects transfer of the labeled phosphate as a modulator compound. The method is useful for identifying compounds that modulate the phosphorylation of human intercellular adhesion molecule polypeptide which might form the basis for the development of therapeutic ambulon diagnostic agents. This sequence represents the humanised mutine antibody ICR-8.1 VK region (HuVK) which is used in the method of the invention
                                                                                                                                                                                                                                                      Identifying modulators of protein kinase C phosphorylation of human intercellular adhesion molecule polypeptide.
                                                                                                                                                                                                                                                                                      Example 14; Col 137-138; 122pp; English.
                                                                                                 92US-00889724.
92US-00894061.
93US-0009266.
93WO-US000787.
93US-00102852.
                                                                   96US-00720420
                                                                                        92US-00827689
                                                                                                                                                                                                  Vazeux R;
                                                                                                                                                                                                                       2000-022778/02.
                                                                                                                                                                            (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                N-PSDB; AAZ24316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 116 AA;
                                                                                                                                                                                                 Gallatin WM,
                                                                                                                                 26-JAN-1993;
05-AUG-1993;
07-JUN-1995;
                                                                  27-SEP-1996;
                                                                                                 26-MAY-1992;
05-JUN-1992;
22-JAN-1993;
                      US5989843-A.
                                            23-NOV-1999
                                                                                       27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
  Mus sp.
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92US-00827689. 92US-00889724. 92US-00894061.

95US-00475680

93US-00009266. 93WO-US000787. 93US-00102852. 94US-00286754.

Vazeux R;

English.

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This invention relates to a hybrid fusion protein comprising an intercellular adhesion molecule (ICAM-R) amino acid fragment at its anno continue and a constant domain of an immunoglobulin heavy chain at its carboxy terminus and a constant domain of an immunoglobulin heavy chain at its carboxy terminus. ICAM-R polypeptides are useful for treating and carboxy terminus. ICAM-R polypeptides are useful for treating and syntheme. Surface, adult respiratory distress syntheme, multiple organ injury synthome secondary to septicaemia or carboxyteme, multiple organ injury of tissue, acute glomerulomephitis, reactive carburitis, dermatosis, stroke, thermal injury, haemodialysis, leukapheresis ulcerative colitis, Crohn's disease, mecroclising enterocolitis, granulocyte transfusion associated syndrome, atheroselerosis and cytokine induced toxicity. ICAM-R polypeptides are specific immune system in a mammal e.g. psoriasis, organ/cissue transplant rejection and autoimmune diseases including Raynaud's syndrome, autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis, diabetes and lupus erythematosus. ICAM-R products and ICAM-R syndrome, autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis, diabetes and lupus erythematosus. ICAM-R products and ICAM-R conducts are also useful in monitoring and treating asthma, tumour growth and/or metastasis, and viral infection (e.g. HIM) infection. Sequences AAA97103-A97112 represent the human ised and ARA97123-A97122 represent CC ICAM-R DNA sequences AAA97113-A97121 and AAA97122-A97122 represent correction of the manised anti-ICAM-R antibody ISC-11, and fragments of the humanised antibody. Sequences AAA97132-A97126 and AAB7132, AAA97132, AAA97134 represent ICR-8: sequences SAA97132, AAA97132, AAA97132, AAA97132, AAA97134 represent ICR-8: sequences SAA97132, AAA97133-A97135 and Indian AAB7132-A97135 and Indian AAB7133-AB7138 and Indian AAB7133-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTWVEIK 116
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Best Local Similarity 88.5 Matches 100; Conservative

61

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RESULT 15

1; Length 116; Indels 89.2%; Score 530.5; DB 3; 88.5%; Pred. No. 4.5e-38; ive 9; Mismatches 3; Conservative Best Local Similarity Matches 100; Conserv

1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 5 DIVWTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF

9 64

SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113

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Anti-human immunodeficiency virus; HIV; cytostatic; ICAM-R; ARDS; stroke; intercellular adhesion molecule; immunoglobulin heavy chain; septicaemia; inflammatory conditions, glomerulonephritis; arthritis; dermatosis; haemodialysis; leukapheresis; ulcerative colitis; Crohn's disease; necrotising enterocolitis; aherosclerosis; psoriasis, asthma; transplant rejection; diabetes; tumour. Protein sequence of humanised ICR-8.1 Vk. AAB13046 standard; protein; 116 AA. 19-DEC-2000 (first entry) AAB13046; 

Search completed: April 18, 2005, 10:00:56 Job time : 65 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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April 18, 2005, 09:57:11; Search time 11.5 Seconds (without alignments) 945.434 Million cell updates/sec Run on:

score: Title: Perfect

US-10-737-208A-1 595 1 DVVMTQTPLSLPVTPGEPAS......SQSTHVPPLTFGAGTKLELK 113 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Id light chain V r	kappa chain pr	chain	kappa chain	kappa cha	kappa chain V	antibody Fab Jel 1	kappa chain V	kappa chain pr	anti-DNA autoantib	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain pre	Ig kappa chain pre	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain V r	Ig kappa chain pre	Ig kappa chain V r	anti-digoxin trans	Ig kappa chain V r	Ig kappa chain pre	Ig light chain V r	Ig kappa chain V r	Ig kappa chain pre				
SUMMARIES	ID	B41940	06	PT0178	S38715	B30577	E27887	853750	PT0359	B34904	PL0205	PL0257	B27887	B32513	C34904	S32189	A27887	D27887	D34904	KVMS26	PH0106	D32530	B31485	C27887	860066	S52449	D29380	S38719	A49715	C29380
	DB	~	~	~	0	0	7	7	~	~	~	7	~	~	~	~	~	~	~	<del>, ,</del>	~	7	~	~	N	~	~	~	7	7
	Query Match Length	113	131	131	115	131	112	112	118	131	113	111	112	131	131	112	112	112	131	113	132	107	112	112	115	131	131	112	112	130
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	Score	40.	35.	535.5	31.	30.	29.	28.	28.	28.	27.	25.	25.	24.	24.	23.	22.	21.	20.	18.	18.	17.	17.	16.	14.	11.	11.	.90	. 90	0
	Result No.		101	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

	chain	Ig light chain pre	chain	chain	chain	chain	chain	chain	kappa chain	kappa chain	light chain	kappa chain	chain	light chain	chain
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PL0203	852028	B39276	S1611	84277	PC420	PH103	E3253	A3180	F2788	\$2633	PH103	A3296	S3886	PH103	R3296
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113 2 PL0203	~	7	~	7	~	0	0	N	~	7	~	0	7	7	0
7	219 2	131 2	219 2	217. 2	219 2	103 2	108 2	112 2	112 2	110 2	103 2	114 2	219 2	103 2	1 6 411
113 2	84.3 219 2	84.1 131 2	84.1 219 2	83.8 217 2	83.8 219 2	83.4 103 2	83.3 108 2	83.3 112 2	82.9 112 2	82.8 110 2	103 2	82.1 114 2	219 2	82.0 103 2	1 C ALL A 18

#### ALIGNMENTS

Ig light chain V region G2b, autoantibody BV04-01 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Ju1-2004
C;Accession: B41940; PL0206
R;Herron, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss - Proteins 11, 159-175, 1991
A;Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional stranded A;Reference number: A41940; MUID:92086633; PMID:1749770

A;Status: preliminary; not compared with conceptual translation
A;Nolecule type: nucleic acid
A;Nolecule type: nucleic acid
A;Cross-references: 1-13 - KHRS.
A;Cross-references: UNIPROT.Q8VCI6
A;Note: sequence extracted from NCBI backbone (NCBIP:70714)
B;Smith, R. G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from PA;Reference number: PL0198; MUID:90309768; PMID:2114528

A; Molecule type: mRNA A; Residues: 1-113 <SMI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin F:16-95/Domain: immunoglobulin homology <IMM>

F;24-39/Region: complementarity-determining 1 F;55-61/Region: complementarity-determining 2 F;94-102/Region: complementarity-determining 3 F;101-113/Region: JH region

Gaps 1; Length 113; Query Match
90.8%; Score 540.5; DB 2; Length 1
Best Local Similarity 93.8%; Pred. No. 6.1e-43;
Matches 106; Conservative 3; Mismatches 3; Indels Query Match Best Local Similarity

1;

9 9 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIXKVSNRF ð

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## RESULT G34903

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F;19-98/Domain: immunoglobulin homology <IMM>
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Title: Active site structure and antigen binding properties of idiotypically cross-real Reference number: A34903; MUD:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig Kappa chain precursor V region (IdBS.7) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Accession: P1019

C;Accession: P1019

C;Accession: P1019

C;Accession: P1019

A;Ferfecti, V; Borden, P; Tao, M.H.; Morrison, S.L.; Kabat, E.A.

Mol. Immunol. 28, 505-515, 1991

A;Ferference mumber: P70174; MUD: 91287738; PMID: 1712074

A;Reference number: P70174; MUD: 91287738; PMID: 1712074

A;Resion: P1018

A;Resion: P1018

A;Resion: P1018

A;Resion: P1019

A;Resion: P1019

A;Resion: Masource: arain BALB/c

C;Comment: IdBS.7 is an antibody to anti-alpha (1-6) dextran.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heteroctetramer; immunoglobulin homology <IMM>
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                            A;Cross-references: GB:M12181; GB:U05237; GB:J05238; NID:g639654; PIDN:AAA61588.1; PID::
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
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A;Accession: S38715
A;Accession: S38715
A;Status: preliminary
A;Status: preliminary
A;Nolecule type: mRNA
A;Residues: 1-115 <CIM>A;Residues: 1-115 <CIM>CIM>CIMO
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38715
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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                                                                                                                                                                                                                                                                                   Length 131;
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                                                                                             A)Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-131 <BED>
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                                                                                                                                                                                                                                                                               90.0%; Score 535.5; DB 92.0%; Pred. No. 2e-42;
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Rikofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof. J. Exp. Med. 161, 805-815, 1985
J. Exp. Med. 161, 805-815, 1985
J. Fille: Genetic elements used for a murine lupus anti-DNA autoantibody are closely relamble A; Reference number: A30577; MUID:85159423; PMID:3920343
A; Accession: B30577
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A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
C;Comment: This squan was determined from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus muscullus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 09-Jul-2004
C;Accession: B30577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region (H146-24B3) - mouse
C;Species: Mus musculus (house mouse)
C;Deceies: D2081 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: E2788 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
Excession: A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
                                                                                                                                                4 DVLWIQTPLSLPVSLGDPASISCRSSQSLVHSNGNIYLHWYLQRPGQSPKLLIYKVSNRF
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                                                                                                                  1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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         Length 115;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                               Indels
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      DB 2;
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      Score 531.5; DB 2
Pred. No. 4.2e-42;
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89.2%; Score 530.5; DB 2.
Best Local Similarity 91.2%; Pred. No. 5.9e-42;
Matches 103; Conservative 4; Mismatches 5
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                                                            6, Mismatches
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Ouery Match
Best Local Similarity 90.3%;
Matches 102; Conservative
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Best Local Similarity
Matches 103; Conserv
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A; Molecule type: DNA
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C'Species: Mus musculus (house mouse)
C'Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C'Accession: PLO257
R'Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
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                                                                                                                                                                                            antibody Pab Jel 103 light chain - mouse C.Species: Wus musculus (house mouse) C.Species: Wus musculus (house mouse) C.Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C.Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C.Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 M.D. Biol. 243, 283-297, 1994 A.T. Li, Y.; Kuderova, A.; Lee, J.; Cygler, M. J. Mol. Biol. 243, 283-297, 1994 A.T. Li, Y.; Kuderova, A.; Lee, J.; Cygler, M. A.T. Lier Preparation, characterization and crystallization of an antibody Fab fragment A.Reference number: S53750; MUID:95018269; PMID:7523684
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DVVMTQTPLSLPVSLGDQAS1SCRSSQSLVHSNGNTYLHWYLQKPGOSPKLL1YKVSNRF
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Species: Mus musculus (house mouse)
Bate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
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J. Exp. Med. 173, 287-296, 1991
A;Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A;Reference number: Pf0352; MUID:91108325; PMID:1988536
                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PYTFGGGTKLEIK 112
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A;Residues: 1-112 <POK>
A;Cross-references: UNIPROT:Q8VCI6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
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B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
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A.Molecule type: mRNA
A.Residues: 1-118 < SHE>
A.Cross-references: UNIPROT: QBVCI6
A.Experimental source: strain BALB/C
C.Comment: This protein is an anti-double-stranded DNA
C.Superfamily: immunoglobulin V region; immunoglobulin P:19-98/Domain: immunoglobulin homology <IMM>
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Matches 103; Conservative
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A;Residues: 1-131 <BED>
A;Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589.1; PID:C
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
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R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Itle: Variable region primary structures of monoclonal anti-DNA autoantibodies from ? A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0205
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C,Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000 C,Accession: B34904; H34903 C,Rccession: B34904; H34903 J.B. Edmundson, A.B.; Voss Jr., E.W. J. Biol. Chem. 265, 133-138, 1990 A,Title: Active site structure and antigen binding properties of idiotypically A,Reference number: A34903; MUID:90094387; PMID:2104617
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb_1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 DVVMTQTPLSLEPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
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A; Residues: 1-113 <SM1.>
A; Residues: 1-113 <SM1.>
A; Cross-references: GB:X53645; NID:g50194; PIDN:CAA37696.1; PID:g930140
C; Superfamily: immunoglobulin 'V region; immunoglobulin homology
F; 16-95/Domain: immunoglobulin homology <IMM>
F; 16-95/Domain: complementarity-determining 1
F; 55-61/Region: complementarity-determining 2
F; 94-102/Region: complementarity-determining 3
F; 101-113/Region: JH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVGAEDLGVYFCSQSTHV-PLTLGAGTKLELK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PWTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1,
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                                                                                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.8%; Score 528.5; DB 2;
larity 91.2%; Pred. No. 9e-42;
Conservative 4; Mismatches 5;
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A;Molecule type: mRNA
A;Residues: 1-131 <BBD.
A;Cross-references: UNIPROT:08VCI6
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
B. BAOL. Chem. 264, 1565-1569, 1989
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi
A;Reference number: A31485; MUID:89109167; PMID:2492278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 DVVMTQTPLSLFVSLGDQASFSCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V region (3-24) - mouse
Cispecies: Wha musculus (house mouse)
Cibate: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
Cibatesion: C34004; I31485
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, I33-139, 1990
A;Title: Active site structure and antigen binding properties of idiotypical A;Reference number: A34903; MUID:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32189
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 DVVMTQIPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                      1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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A; Molecule type: DNA
A; Residues: 1-131 < KOF;
A; Cross-references: GB: M20828; NID:g196937; PIDN: AAA38843.1; PID:g196938
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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                                                                                                                                                                                                                                                                  Length 131;
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A;Molecule type: protein
A;Residues: 20-52 <BE2.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                           88.2%; Score 524.5; DB 2; 90.3%; Pred. No. 2.1e-41; ive 5; Mismatches 5;
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submitted to the EMBL Data Library, February 1993
submitted number: S32185
A;Accession: S32189
A;Accession: S32189
A;Seatus: preliminary
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
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Best Local Similarity
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Best Local Similarity
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19 #52513
19 kappa chain precursor V region (MRL4) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: B32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa 11ght chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
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'Species: Mus musculus (house mouse)
'Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
'Accession: B27887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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                                                                                          Cross-references: UNIPROT: 08VCI6 Superfamily: immunoglobulin homology Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 525.5; DB 2
Pred. No. 1.4e~41;
5; Mismatches 4
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F;40-54/Region: framework 2
F;55-61/Region: framework 3
F;62-93/Region: framework 3
F;41-102/Region: framework 4
F;103-111/Region: framework 4
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Matches 102; Conservative
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A;Cross-references: EMBL:X70094; NID:g288255; PIDN:CAA49699.1; PID:g288256 (S.Ugerfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology < IMM> P;16-95/Domain: immunoglobulin homology < IMM>
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Query Match 88.0%; Score 523.5; DB 2; Length 112; Best Local Similarity 90.3%; Pred. No. 2.2e-41; Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;  1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60  1 DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60		,		
Y Match 88.0%; Score 523.5; DB 2; Length 112; Local Similarity 90.3%; Pred. No. 2.2e-41; Indels 1; Gaps: hes 102; Conservative 4; Mismatches 6; Indels 1; Gaps: 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF   1 DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIHKVSNRF 1 DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF		1;	09	
98.0%; Score 523.5; DB 2; Length 112; Local Similarity 90.3%; Pred. No. 2.2e-41; hes 102; Conservative 4; Mismatches 6; Indels 1; 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIH 1 DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIX 1 DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIX		Gaps	KVSNRF        KVSNRF	
y Match 88.0%; Score 523.5; DB 2; Length Local Similarity 90.3%; Pred. No. 2.2e-41; Indels 102; Conservative 4; Mismatches 6; Indels 1 DVWHQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQS   1 DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQS	112;	1,	PKLLIH      : PKLLIY	
y Match 1. Local Similarity 90.3%; Pred. No. 2.2e-41; 1. Local Similarity 90.3%; Pred. No. 2.2e-41; 1. Local Similarity 90.3%; Pred. No. 2.2e-41; 1. Lovy Conservative 4; Mismatches 6; 1. DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHW 1. DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHW 1. DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHW	Length	Indels	YLOKPGOS           YLOKPGOS	
4 5 6	Query Match 88.0%; Score 523.5; DB 2; Best Local Similarity 90.3%; Pred. No. 2.2e-41;	ches 102; Conservative 4; Mismatches 6;	1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHW	

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April 18, 2005, 09:42:15; Search time 84.5 Seconds (without alignments) 684.792 Million cell updates/sec
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595
1 DVVMTQTPLSLPVTPGEPAS......SQSTHVPPLTFGAGTKLELK 113
GenCore version 5.1.6
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Database

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KV3B MOUSE
KV3N MOUSE
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Q65ZII
KV3B MOUSE KV2C\_MOUSE KV2A\_MOUSE KV1\_CANFA HUMAN HUMAN MOUSE MOUSE KV2G MOUSE KV2A HUMAN KV2B HUMAN Query Match Length DB 9198.5 Š. Result

86         2         Q723Y5         homo sapien           111         1         KV3H_MOUSE         Q64D18 homo sapien           236         2         Q64D18 homo sapien         Q64D18 homo sapien           111         1         KV3K_MOUSE         P01663 mus musculu           111         1         KV3M_MOUSE         P01675 mus musculu           111         1         KV3O_MOUSE         P01677 mus musculu           111         1         KV3O_MOUSE         P01677 mus musculu           109         1         KV3D_MOUSE         P01672 mus musculu           109         1         KV3D_MOUSE         P01622 homo sapien           110         1         KV3P_MOUSE         P01668 mus musculu           10         1         KV3P_MOUSE         P01670 mus musculu           235         2         Q6GW79         P01670 mus musculu           111         1         KV3L_MOUSE         P01670 mus musculu           111         1         KV3L_MOUSE         P01664 mus musculu	ALIGNMENTS	STANDARD; PRT; 113 AA.	21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig kappa chain V-II region 26-10.	Mus musculus (Mouse). Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCDI_TaxID=10090;	Sles M.N.; bubwed=6404298; Snce of the light chain variable region from a mouse	ridoma antibody."; 1153-1158(1983). Si This Chain was isolated from an IgG2a hybridoma binds digoxin.	PIR, A01914; KVMS26. HSSP, Og9M37; IIS InterPro; IPR00110; Ig-like. InterPro; IPR003596; Ig-v.	73; 1. [Gv.] 1. ; IG_LIKE; 1. equencing; Hybridoma; Immunoglobulin V region;	Framework-1. 39 Complementarity-determining-1. 54 Framework-2.	61 Complementarity-determining-2. 93 Framework-3. 102 Complementarity-determining-3. 112 Framework-4. 93 By similarity.	A; 12273 MW; F9F39CE949A84C2A CRC64; 87.1%; Score 518.5; DB 1; Length 113; Y 88.5%; Pred. No. 2.4e-46; srvative 7; Mismatches 5; Indels 1; Gaps 1.	DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60 	SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFCAGTKLELK 113 
0.000 0.000			86 (Rel. 0 86 (Rel. 0 04 (Rel. 4 chain V-II	Mus musculus (Mouse) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;	J; 3178921; P ., Margoli id sequenc	xin hybrid try 22:115 LLANEOUS: in that bi	14, KVMS26 M37, 1191. IPR007110 IPR003596	0047; ig; 00406; IGv PS50835; I otein segu	24 40	25 103 103 123	A;	DVVMTQTPLS          DVVMTQTPLS	SGVPDRFSGS            SGVPDRFSGS
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Pfam; PF07654; C1-set;
SMART; SM00409; IG; 2
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SEQUENCE 513505; bubMedes 9768802;

MEDINE-52431950; bubMedes 9768802;

WA Kipp B., Schlaak M., Becker W.M.,

"Cloning and expression of a recombinant mouse Fab-fragment

Trecognizing a defined linear epitope of Chironomus thummi major

Transparenchi t.";

Int. Arch. Allergy Immunol. 110:348-353(1996).

REMBL, 237499; CAA8574.1;

Int. Arch. Allergy Immunol. 110:348-353(1996).

REMBL, 237499; CAA8574.1;

InterPro; IPR0031599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003596; Ig.

InterPro; IPR00359
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MEDLINE=92020904; PubMed=1924323;
Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.,
"B3 (Fv)-PE38KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice.";
Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10095;
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                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kappa light chain C region (Fragment).
Mus musculus (Mouse).
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Last annotation update)
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85.8%; Pred. No. 1.7e-43;
live 7; Mismatches 8;
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SMART; SMO0407; IGc1; 1.
PROSITE; PSS0835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
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065207;
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25-0CT-2004 (TrEMBLE1. 28, L.
25-0CT-2004 (TrEMBLE1. 28, L.
25-0CT-2004 (TrEMBLE1. 28, L.
B3 (FV). PE40 (Fragment).
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Matches 97; Conservative
                                                PRELIMINARY;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X TISSUB=Lung;
X Strausberg R.L., Faingold B.A., Grouse L.H., Derge J.G.,
Atrausberg R.L., Faingold B.A., Grouse L.H., Derge J.G.,
Atrachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parner A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parner A.A., Rubin G.M., Hong L.,
A Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninol P.H.,
Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
A Hilaton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Richards S.J., Marra M.A.,
A Jones S.J., Marra M.A.,
Tones S.J., Marra M.A.,
Tones S.J., Marra M.A.,
Tones S.J., Marra M.A.,
Tones G.J., Marra M.A.,
The Manan D. S., Marra M.A.,
Tones S.J., Marra M.A.,
Tones G.J., Mallalysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR003599; IG.
InterPro; IPR00310; IG-like.
InterPro; IPR00310; IG-like.
Ffam; PF00047; ig; 2.
SWART; SW00409; IG; 2.
PROSITE; PS50839; IG LIKE; 2.
ROWITE; PS50839; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 248 AA; 26634 MW;
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003066; Ig.MIC.
InterPro; IPR003596; Ig.V.
Pfam. PR07654; CI-884; I.
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1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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J. Clin. Invest. 52:1276-1281(1973).
J. Clin. Invest. 52:1276-1281(1973).
J. MISCELLANEOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.
J. MISCELLANEOUS: This protein was isolated from the urine of a patient with plasma cell dyscrasia and amyloidosis.
J. MISCELLANEOUS: The C region of this chain has the INV (1,2)
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                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                      SEQUENCE (BENCE-JONES PROTEIN TEW).
MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acide sequence of a kappa Bence Jones protein from a case primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
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GO; GO:00058276; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Fram; PR00407; ig-y.
Fram; PR00407; ig-y.
PR087TE; PS50835; IG_LIKE; 1.
PR097TE; PS50835; IG_LIKE; 1.
Amyloid; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
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SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
MEDLINE-73166638; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
Glenner G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12316 MW; 0C3C38F81F1843CA CRC64;
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Last sequence update)
Last annotation update)
21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig kappa chain V-II region TEW.
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01-JUN-2002 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
Hypothetical protein.
Homo sapiens (Human).
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Q8TCD0
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                                                                                                                                                                                              1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRP
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                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                      78.2%; Score 465; DB 2; Length 240; 77.9%; Pred. No. 2.3e-40; ive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.0%; Score 464; DB 2; Length 11 Best Local Similarity 77.9%; Pred. No. 1.2e-40; Matches 88; Conservative 13; Mismatches 12; Indels
                                                                    Hypothetical protein.
SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035034; AAD56270.1; -.
PIR; B49002; B49002.
PIR; S23638; S23638.
PIR; S34094; S34094.
PIR; S34095; B74095.
HSSP; P01625; ILVE.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-v.
SMART; SM00406; IGv; 1.
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              SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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P01617;
21-JUL-1986 (Rel. 01, Created)
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01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                        Local Similarity 77.9 tes 88; Conservative
 SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE
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KV2D_HUMAN
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TISSUE-LUNG;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

METAUSDER R.D., Feingold E.A., Grouse L.H., Derge J.G.,

MALTAGENIS R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MALTAGENIS R.D., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

MAISCHIS S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.K.,

MAISCHORKO L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MALTAGEN M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MALTAGEN B.A., McEwan P.J., McKernan K.J., Malz M.A., Gay L.J., Hulyk S.J.,

MALTAGEN S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Markelley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Markelley R.W., Touchman J.W., Green E.D., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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    Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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PIR; 540324; 540324.
PIR; 540324; 540324.
PIR; 542267; 542267.
PIR; 542268; 542268.
INCEPPO; IPR007110; Ig-like.
INCEPPO; IPR003197; Ig cl.
INCEPPO; IPR003595; Ig Cl.
INCEPPO; IPR003596; Ig WHC.
INCEPPO; IPR003596; Ig WHC.
PEAM; PF07654; Cl-eet; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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PIR, S34095; S34095
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                                                                                SEQUENCE FROM N.A.
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Matches
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Q6P491
ID Q6P4
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DT 0S-J
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A STEADESEKIN;

XE STEADESEKIN;

XE STAUSSERSEST;

YELDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XE STAUSSERSEST; PubMed=12477932; DOI=10.1073/pnas.242603899;

XE STAUSSERSEST; PubMed=12477932; DOI=10.1073/pnas.242603899;

XE STAUSSERSER R.D., Celling F.S., Magner L., Shanman C.M., Schuler G.D.,

RA Altachul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,

Rab Sares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rab Brownstein M.J., Vadin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Broak S.A., McKenn P.J., McKernan K.J., Malek J.A., Gavia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muray D.W., Sodergen B.J., Lu X., Gibbs R.A.,

RAP Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Tornershinki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Mones S.J., Marra M.A.,

R. Tellon and initial analysis of more than 15,000 full-length human
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    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG63599; AAH63599.1; -.
HSSP; P01837; 1KCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835, IG_LIKE; 2.
PROSITE; PS00230; IG_MHC; UNKNOWN_1.
Hypothetical protein_2
SEQUENCE 239 AA; 26245 WW; CD7313DDFFD358B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.6%; Score 455.5; DB 2; Best Local Similarity 75.2%; Pred. No. 2.2e-39; Matches 85; Conservative 15; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003596; Ig wr.
InterPro; IPR003596; Ig w.
Pfam; PF07654; C1-set; I.
SMART; SM00407; IG.
SMART; SM00407; IGC1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                SEQUENCE FROM N.A.
                                        NCBI_TaxID=9606
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KV2E_HUMAN
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Last sequence update) Last annotation update)

05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Homo sapiens (Human).

Q6P491;

Created)

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Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHW-SWTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-II region RPMI 6410.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Prostate; MbMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.2%; Score 453.5; DB 1; Length 133; 77.9%; Pred. No. 1.8e-39; ive 13; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity-determining-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          EMBL, Z00020; CAA77315.1; -. PTR; A01890; KZHURP.
HSSP; Q99M37; 1191.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000555; F:antigen binding; NAS.
GO; GO:000555; P:immune response; NAS.
InterPro; IPR007100; IG-like.
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Nucleic Acids Res. 13:6499-6513(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
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Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                               MEDLINE=84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kappa chain V-II region GM607.
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Framework-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12664 MW; 92C57DC719E558B1 CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z00009; -; NOT_ANNOTATED_CDS.
PIR; A01889; K2HUGM.
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SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regIon; Signal.
NON_TER 1
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Matches 88; Conservative
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                                                                                                                                             diversity.";
Nature 309:73-76(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99M37; 119I.
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SEQUENCE
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DVVMTQTPLSLPVTPGEPASISCRSSQSLVHR-NGNTYLHWYLQKPGQSPKLLIHKVSNR
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"Variable region sequence of the light chain from a Waldenstrome IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
I- MISCELLANEOUS: This of hain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
PIR; A01886; KZHUFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                      Length 115;
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Complementarity-determining-3.
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                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                           115 AA; 12676 MW; 59E9F90A379569EC CRC64;
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                                                 GG; GO: 0005576; C: extracellular; NAS.
GG; GO: 0003823; F: antigen binding; NAS.
GG; GO: 0005852; F: antigen binding; NAS.
INTERPO: IPRO(310); III-like.
InterPro; IPRO(310); III-like.
InterPro; IPRO(310); III-like.
FRAMAR; SMO(406; IGV; I.
PROSITE; PSSO(835; IG_LIKE; I.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
DISULPID 24 95 similarity.
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                                                                                                                                                                                                                                                                                                                                74.6%; Score 444; DB 1; L. 76.3%; Pred. No. 1.5e-38; ive 13; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 01, Last sequence update)
(Rel. 44, Last annotation update)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=76253627; PubMed=821524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seques OS-JUL-2004 (Rel. 44, Last anno IS kappa chain V-II region FR. Homo sapiens (Human).
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les 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                PIR; B91639; K2HUCM
HSSP; P01751; 1NQB.
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P01615;
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SEQUENCE
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SEQUENCE
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Xrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilschmann N.; "The complete amino acid sequence of Bence Jones protein Cum (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                               Strausberg R.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC030814, AAH30814.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26024 MW; F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.1%; Score 452.5; DB 2
76.1%; Pred. No. 4.6e-39;
ive 12; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 Appa chain V-II region Cum.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00230; IG_MHC; UNKNOWN_1.
Hypothetical protein
SEQUENCE 239 AA; 26024 MW; F5E20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=70063440; PubMed=4188189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=68242259; PubMed=5586923;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003506; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PR07654; Cl-set; I.
SWART; SW00406; IGv; I.
                                                                                                                                                                                and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.1#
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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PIR; S40357; S40357.
HSSP; P01834; 117Z.
                                                                                                                                                                                                                                                                                                                                        PIR; S23638; S23638
PIR; S34091; S34091
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Prostate;
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KV2A HUMAN P01614;

RESULT 12 KV2A HUMAN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
  musculus (Mouse)
                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                             Dreyer W.J., Gray W.R., Hood L.E.;

The genetic, molecular, and callular basis of antibody formation:

The genetic, molecular, and callular basis of antibody formation:

Toome facts and a unifying hypothesis.

Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).

-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

-!- MISCELLANEOUS: This is a Bence-Jones protein.

PIR; A01887; KZHUML.

R HSSP; Q99M37; 1191.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR001596; Ig-v.

R Fam; PR0047; ig, 1.

R PROSITE; SWO0406; IGv; 1.

R PROSITE; PS50815; IG_LIKE; 1.

W Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPK1LIHKVSNRF
             1; Gaps
                                                                                                                                                                                                                                                                                                                                                marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                             61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.6%; Score 426; DB 1; Length 11
69.0%; Pred. No. 1.1e-36;
ive 21; Mismatches 12; Indels
           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12055 MW; E5B22E2FA7ABE481 CRC64;
 Pred. No. 3.4e-38;
                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Homo sapiens (Human).
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-2094 (Rel. 01, Last sequence update)
19 kappa chain V-II region 7534.1.
          13; Mismatches
                                                                                                                                                           112 AA
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                                                                                                                                                         PRT;
75.2%;
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           85; Conservative
                                                                                                                                                           STANDARD;
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112 AA;
Best Local Similarity
                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                           KV2C_HUMAN
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SEQUENCE.
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SEQÜENCE
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KV2F_MOUSE
                                                                                                                                               KV2C HUMAN
           Matches
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MEDLINE=81256427; PubMed=6409088;

MEDLINE=81256427; PubMed=6409088;

The Chains from a mouse hybridoma-derived anti-(streptococcal group of the diants from a mouse hybridoma-derived anti-(streptococcal group of polysaccharide) antibody containing an additional cysteine residue.

The A polysaccharide) antibody containing an additional cysteine residue.

The Application of the dimethylaminoazobenzene isothiocyanate technique of the isolation of peptides.";

E hochem. J. 211:173-180(1983).

E his chains the streptococcal group A polysaccharide.

The Application of peptides.";

E hichem. J. 211:173-180(1983).

E his polysaccharide.

The Application of peptides.";

E hichem. J. 211:173-180(1983).

E hichem. J. 211:173-180(1983).

The Application of peptides.";

E hichem. J. 211:173-180(1983).

E hichem. J. 211:173-180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVBAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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Complementarity-determining-1.
Pramework-2.
Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity
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Les 80; Conservative
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536.541 Million cell updates/sec
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595
1 DVWMQTPLSLPVTPGEPAS.....SQSTHVPPLTFGAGTKLELK 113
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
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| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 689, App	Sequence 2020, Ap	Sequence 687, App	Sequence 2018, Ap	Sequence 18, Appl	Sequence 675, App	Sequence 2006, Ap	Sequence 66, Appl	Sequence 66, Appl	Sequence 29, Appl	Sequence 29, Appl	Sequence 685, App	Sequence 2016, Ap
ID	US-10-468-370-689	US-10-468-496-2020	US-10-468-370-687	US-10-468-496-2018	US-10-762-629-18	US-10-468-370-675	US-10-468-496-2006	US-09-753-436-66	US-10-163-942-66	US-10-372-481-29	US-10-371-797-29	US-10-468-370-685	US-10-468-496-2016
рв	15	16	15	16	16		16			15	15	15	16
* Query Match Length DB ID	113	113	113	113	114	113	113	116	116	139	139	113	113
Query Match	95.8	95.8	93.8	93.8	91.9	89.4	89.4	89.2	89.2	89.0	89.0	88.4	88.4
Score	570	570	558	558	547	532	532	530.5	530.5	529.5	529.5	526	526
Result No.	-	7	m	4	Ŋ	9	7	80	σ	10	11	12	13

Sequence 22, Appl		35,	42,	20,	47,	48,	49,		201	4	Sequence 4, Appli	4,	61	4, A	Ψ	2012		Sequence 2010, Ap	Sequence 3, Appli	Sequence 27, Appl	Sequence 677, App	8	Sequence 95, Appl	Sequence 2, Appli	4	26	'n	Sequence 6, Appli	2	8	8
US-10-741-657A-22	US-10-741-657A-14	US-09-726-	US-09-726-	US-10-741-	US-10-235		US-1	US-10-468-370-6	US-1	US-09-518-737-4	US-10-723-748	US-09-887-853-4	ns-	-Su	US-10-468-370-681	US-10-468-496-2	-sn	US-10	US-10-270-555-3	US-10-687-035-27	US-10-468-370-677	US-10-468-496-2008	-SU	ns-	US-09-726	US-10-258-728-2	US-10-919	US-10-138-			US-10-257-864A-87
16	16	-	10	Н	Н	***	٦	~	16	-	Н	9	15	Ч	15	٦	15	H	14	. 17	15	-	Н		4	15	Н	. 14	H	7	12
112	112	131	242	112	507	510	510	113	113	112	112	252	132	252	113	113	113	113	474	131	113	113	131	131	114	112	112	131	131	13	131
8.3	8.0	88.0	0.8	٠	7.8	ζ.	7.8	7.4	87.4	7.1	7.1	7.1	7.0	9.9	9.9	9.9	1.9	6.1	0.9	5.6	5.4	85.4	5.3	5.3	5.0	4.8	4.8	4.8	4.8	4.8	4.8
80					60																							æ	 	8	8
525.5	523.5	523.	523.5	522.	522.	522.	522.	52(	520	518.5	518.	518.	517.5	515.	515	515	51;	517	511.5	509.	505	508	507.	507.	206	504.5	504.	504.5	504.5	504.	504.
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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US-10-469-370-689

US-10-469-370-689

Sequence 689, Application US/10468370

Publication No. US20040082039A1

GENERAL INFORMATION:
APPLICANT: Gailies, Stephen
APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Maxian
APPLICANT: Hamilton, Maxian
APPLICANT: Walliams, Stephen
APPLICANT: Watthew, John
APPLICANT: LING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
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PRIOR APPLICATION NUMBER: EP 01108291.4
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PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR PILI
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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                                      APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Williams, Anita
APPLICANT: Williams, Anita
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: METHOD FOR IDENTIFICATION NUMBER: US/10/468,496
CURRENT APPLICATION NUMBER: 0110354.2
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR APPLICATION NUMBER: 01106538.4
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR FILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR FILING DATE: 2001-03-15
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                                                                                           1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRP
                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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        Gaps
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                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSGSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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95.8%; Score 570; DB 16; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.6e-45;
Matches 109; Conservative 2; Mismatches 2; Indels
        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MHC class II binding epitope
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2020
LENGTH: 113
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APPLICANT: Garr, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Carrer, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                   Sequence 2020, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-468-496-2020
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APPLICANT: Baker: Mattiew: Mat
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Sequence 2006, Application US/10468496

j Sequence 2006, Application US/10468496

j Publication No. US20040180386A1

gENERAL INFORMATION:

j APPLICANT: Carter, Francis J.

APPLICANT: Garter, Graham

j APPLICANT: Marity Frequency

TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL

TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL

TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL

TITLE OF INVENTION: IMMUNOGENCITY

FILE REPERENCE: MER.117

CURRENT PLIJNG DATE: 2003-09-25

PRIOR PILING DATE: 2001-03-19

PRIOR PLILING DATE: 2001-03-16

PRIOR PELING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-15

PRIOR PILING DATE: 2001-03-05

PRIOR PILING DATE: 2001-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLTISRLEAEDLAVYFCSQSTHVPPLTFGQGTKLEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 89.4%; Score 532; DB 15; Best Local Similarity 89.4%; Pred. No. 5.6e-42; Matches 101; Conservative 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 532; DB 16;
Pred. No. 5.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: MHC class II binding epitope US-10-468-370-675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THER INFORMATION: MHC class II binding epitope
                          FILE REFERENCE: MER-116
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
FRIOR APPLICATION NUMBER: EP 01103955.9
FRIOR FILING DATE: 2001-02-19
FRIOR FILING DATE: 2001-05
FRIOR PILING DATE: 2001-05
FRIOR APPLICATION NUMBER: PCT/EP02/01690
FRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2006
   IMMUNOGENICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.4%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                         1 DVVMTQTPGSLPVSAGDQASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDSGVYFCSQSTHVPPLTFGAGTKLELK 113
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APPLICANT: Abdel-Meguid, Sherin
APPLICANT: Abdel-Meguid, Sherin
APPLICANT: Abdel-Mess. Stephen D.
APPLICANT: How You Sen
TITLE OF INVENTION: Alexander H.
TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
FILE REFERENCE: P5087
CURRENT APPLICATION NUMBER: US/10/762,629
CURRENT APPLICATION NUMBER: US/09/914,695
PRIOR APPLICATION NUMBER: US/09/914,695
PRIOR PILING DATE: 2001-08-31
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 114
                                                                                           Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
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APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: Bay, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 547; DB 16;
Pred. No. 2.3e-43;
4; Mismatches 5;
                                                                                        Query Match
93.8%; Score 558; DB 16;
Best Local Similarity 94.7%; Pred. No. 2.1e-44;
Matches 107; Conservative 2; Mismatches 4;
OTHER INFORMATION: MHC class II binding epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 675, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Garr, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/10762629
Publication No. US20040141964A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.0%;
Matches 104; Conservative
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      ; US-10-468-496-2018
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Length 113;

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Length 113;

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us-10-737-208a-1.rapb

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1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                               5 DIVMTQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                   65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGGGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402 COWPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OF COMPATIBLE OF COMPATIBLE STATEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                Score 530.5; DB 9; Length 116;
Pred. No. 7.9e-42;
9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE: «Unknown»
APPLICATION NUMBER: 09,382,289
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-UNN-1995
APPLICATION NUMBER: US 08/286,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-ANN-1993
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-ANN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APELICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/163,942
FILING DATE: 05-Jun-2002
CLASSIFFCATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/889,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., CREGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/10163942
Publication No. US20030199423A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (312) 474-0448
                                                           Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
          JS-09-753-436-66
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-163-942-66
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                                                                                      DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
          0; Gaps
                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLTISRLEABDLAVYFCSQSTHVPPLTFGQGTKLEIK 113
                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
FILING DATE: 05-MG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-MG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-WAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 26-WAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-UN-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-UN-1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-UN-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    Sequence 66, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 116 amino acids
amino acid
     Conservative
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     101;
Matches
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TYPE: PRT
CORGANISM: homo sapiens
US-10-371-797-29
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       LENGIH: 139
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 29, Application US/10372481

Sequence 29, Application No. US20030202975A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES

FILE REFERENCE: 5405.306

CURRENT FAPLICATION NUMBER: US/10/372,481

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: PCT/US03/05549

PRIOR FILING DATE: 2003-10-21

PRIOR FILING DATE: 2002-10-21

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.2

TYPE: PRIOR

TYPE
                                                                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                             Gaps
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                                                                                                     DB 14; Length 116;
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Publication No. US20040001828A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TUSCANO, JOSEPh
APPLICANT: TEDDER. Thomas
TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 39754-0951
CURRENT APPLICATION NUMBER: US 60/420,472
PRIOR FILING DATE: 2002-10-21
PRIOR PLICNION NUMBER: US 60/420,472
PRIOR PLICNION NUMBER: US 60/359,419
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                 Score 530.5; DB 14;
Pred. No. 7.9e-42;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.0%; Score 529.5; DB 15; Best Local Similarity 91.2%; Pred. No. 1.2e-41; Matches 103; Conservative 4; Mismatches 5;
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-163-942-66
                                                                                                 Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-372-481-29
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US-10-372-481-29
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20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
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                                                                                                             1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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Query Match 89.0%; Score 529.5; DB 15; Length 139; Best Local Similarity 91.2%; Pred. No. 1.2e-41; Matches 103; Conservative 4; Mismatches 5; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THER INFORMATION: De-immunized MHC class II binding epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

88.4%; Score 526; DB 15; Length 1:
Best Local Similarity 86.7%; Pred. No. 2e-41;
Matches 98; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Matkins, John
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Way, Jeffrey
ITILE OF INVENTION: INMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
ITILE OF INVENTION: IMMUNOGENICITY
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT APPLICATION NUMBER: EP 01103955.9
FRIOR PILING DATE: 2001-02-19
FRIOR APPLICATION NUMBER: EP 01108291.4
FRIOR PILING DATE: 2001-04-05
FRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 685
ILENATH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2016, Application US/10468496 Publication No. US20040180386A1 GRNERAL INFORMATION: APPLICANT: Carr, Francis J.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 685, Application US/10468370 Publication No. US20040082039A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamilton, Anita
Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gillies, Stephen APPLICANT: Carr, Francis J. APPLICANT: Jones, Tim APPLICANT: Carter, Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanlon, Marian
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61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHL-PWTFGGGTKLEIK 112
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ORGANISM: Mus sp.
                                                                                                  RESULT 15
US-10-741-657A-14
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                          APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: IMMUNGEBROITY
FILE OF INVENTION: IMMUNGEBROITY
TITLE OF INVENTION: IMMUNGER: US/10/468,496
TITLE OF INVENTION: IMMUNER: 01103954.2
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 01105777.5
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-20
PRIOR PILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLTISRLEAEDMAVYFCSQSTHVPPLTFGGGTKVEIK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14

US-10-741-657A-22

US-10-741-657A-22

SQUEDICE 22, Application US/10741657A

Publication No. US20040197325A1

GENERAL INPOWATION:

TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF

TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/741,657A

CURRENT FILING DATE: 2003-12-19

NUMBER OF SEQ ID NOS: 300
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Pred. No. 2.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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SEQ ID NO. 22
LENGTH: 112
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Best Local Similarity 90.3%;
Matches 102; Conservative
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Best Local Similarity 86.74
Matches 98; Conservative
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; ORGANISM: Mus sp.
US-10-741-657A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PWTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 112;
Sequence 14, Application US/10741657A
Publication No. US20040197325A1
GENERAL INRORMATION:
APPLICANT: Protein Design Labs
TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/741,657A
CURRENT FILING DATE: 2003-12-19
NUMBER: OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.2
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 523.5; DB 16; Length
Pred. No. 3.4e-41;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 18, 2005, 10:17:26
Job time : 71 secs
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Best Local Similarity 90.3
Matches 102; Conservative
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Sequence 4, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: HONEGGER, ANNEWARIE
TITLE OF INVENTION: INMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
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                       Sequence
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Sequence
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Sequence
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Patent No. 6706487

GENERAL INFORMATION:
APPLICANT: Abdel-Meguid, Sherin
APPLICANT: Ho, Yen Sen
TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
TITLE OF INVENTION: Recombinant of IL-18 Mediated Disorders
TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
FILE REFERENCE: P50897

CURRENT APPLICATION NUMBER: US/09/914,695

CURRENT APPLICATION NUMBER: PCT/US00/07349

PRIOR FILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-03-17

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 48

NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.9%; Score 547; DB 4; Length 114; 92.0%; Pred. No. 7.4e-46; ive 4; Mismatches 5; Indels
US-09-08-444A-42
US-09-026-985-42
US-09-211-952A-42
US-09-214-340A-42
US-09-518-737-4
US-08-257-341-7
US-08-257-341-7
US-08-461-838-4
US-08-461-838-4
US-08-257-341-5
US-08-224-591-12
US-08-224-591-12
US-08-224-591-12
US-08-226-789-12
US-09-166-093-21
US-09-166-093-21
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Best Local Similarity 92.0°
Matches 104; Conservative
                                           ORGANISM: Mus musculus
    888.00
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US-09-914-695-18
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US-09-232-290-4
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                                                                                                                                                                    (without alignments)
443.965 Million cell updates/sec
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                                                                                                                                               April 18, 2005, 09:57:36; Search time 19 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Barlorus_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Pcrus_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-482-882-66
US-08-487-113D-66
US-08-487-113D-66
US-08-473-503-66
US-08-720-4203-66
US-08-714-017-66
US-08-714-017-66
US-08-73-14-017-66
US-08-378-14106-61
US-08-388-6113-48
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US-08-388-6113-48
US-08-077-449-35
US-09-077-449-35
US-09-0111-9553-35
US-09-111-9553-35
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US-08-398-612A-56
US-08-398-611A-56
US-08-491-334A-56
US-09-027-449-42
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                                                                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                             US-10-737-208A-1
595
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                                                                                                        OM protein
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Gaps

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| REGISTRATION NUMBER: P-41,337 | REGISTRATION NUMBER: 27866/; | TELECOMUNICATION INFORMATION: | TELEFONE: (312) 474-6300 | TELEFAX: (312) 474-640 | TELEFAX: (312) 474-640 | TELEFAX: (312) 474-600 | INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 89.2%;
       I'ELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 116 ami-
                   (312) 474-0448
                                                                                                            : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                      Best Local Similarity 88.5 Matches 100; Conservative
                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Suh, Young J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-483-389-66
                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                1 DVWMTQTPLSLPVSLGPQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                          1; Gaps
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                                                                                                                                                                                                                                                                                            Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-482-882-66;

Sequence 66, Application US/08482882;
Patent No. 577318;
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Nosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods;
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Matchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STREET: 111inois
CUUNRY: USA
                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRIES 60606

ZIP: 60606

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                       Score 533.5; DB 4;
Pred. No. 1.5e-44;
3; Mismatches 4;
CURRENT APPLICATION NUMBER: US/09/232,290A CURRENT FILING DATE: 1999-01-15 EARLIER APPLICATION NUMBER: PCT/EP96/02230 EARLIER FILING DATE: 1996-05-23 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-A0C-1993
FILING DATE: 05-A0C-1993
FRICH APPLICATION NUMBER: US 08/102,852
FILING DATE: 22-DN-1993
FRICH APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-DN-1993
FRICH APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-AUN-1992
FRICH APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 26-MAY-1992
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-AN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5773218AND, 35022
BREGESPANCE NUMBER: 35,3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32178 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.9%;
Matches 105; Conservative
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                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-4
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                                                                                                                                                                        113
                                                                                                                                              SEQ ID NO 4
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5 DIVMIQSPLSLPVIPGEPASISCRSSQSLVHSNGDIYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                                  1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                               Gaps
                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                    65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                               Ή,
Score 530.5; DB 1; Length 116; Pred. No. 3e-44;
                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALDRESSES: MAISBAIL, O'10016, GESBUELL, MUKESSES, STREET: 233 SOUTH WACKET DIIVO/6500 GEARS TOWER STATE: Illinois
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
21P: 60606
COMPUTER: EDGENE: BENEVILLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/483,389
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING APPLICATION NUMBER: US 08/102,865
FILING APPLICATION NUMBER: US 08/009,266
FILING APPLICATION NUMBER: US 07/894,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66, Application US/08483389
Patent No. 5811517
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/08487113D

Patent No. 5837822

GENERAL INPORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods
ITITE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 66606-6402

COUNTRY: United States of America
STATE: Illinois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy daish
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CONFORTER: IBM PC COMPATIBL
                                                                                                                                                                                                                                                                                                                         Length 116;
                                                                                                                                                                                                                                                                                                                    Score 530.5; DB 2;
Pred. No. 3e-44;
9; Mismatches 3;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,113D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-AUM-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-AUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5837822AAG, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
           116 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 amino acids
                                                        ; TYPE: amino acid
; TOPOLOGY: lineár
; MOLECULE TYPE: protein
US-08-483-389-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-487-113D-66
LENGTH:
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                                                                                                                                                                                                                      5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                         Query Match

89.2%; Score 530.5; DB 2; Length 116;
Best Local Similarity 88.5%; Pred. No. 3e-44;
Matches 100; Conservative 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66, Application US/08483932
Patent No. 5880268
GENERAL INPORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
TUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Galo Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,932
FILING DATE: 07-JUN-1995
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 05-AUG-1993
PRIOR APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 22-JAN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 25-MAN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 25-MAN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 25-MAN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 35-MAN-1992
PRIOR APPLICATION NUMBER: 35,302
RESERRENCE/DOCKET NUMBER: 32.798
TELECOMMUNICATION INTORMATION:
TELECOMMUNICATION INTORMATION:
TELECOMMUNICATION INTORMATION:
TELECOMMUNICATION INTORMATION:
TELECOMMUNICATION INTORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 66:
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
; MOLECULE TYPE: protein US-08-473-503-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein US-08-483-932-66
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1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                       Gaps
                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                        65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                       ۲,
Query Match 89.2%; Score 530.5; DB 2; Length 116; Best Local Similarity 88.5%; Pred. No. 3e-44; ... Matches 100; Conservative 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,420A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illingis
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAONE: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (312) 474-6300
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1 DVVWTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                         5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRP
                                                                                                                                                                                                                                                                        65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                              Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66, Application US/08475680
Patent No. 6100383
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: 11linois COUNTRY: 11linois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUW TYPE: FLOPPY disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/475,680 FILING DATE: 07-UNN 1995 CLASSIFICATION: 530
                            89.2%; Score 530.5; DB 3;
88.5%; Pred. No. 3e-44;
ive 9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.2%; Score 530.5; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 26-MAY-1992
FILING DATE: 26-MAY-1992
FILING DATE: 27-JAN-1992
FILING DATE: 27-JAN-1992
FILING DATE: 27-JAN-1992
FILING DATE: 37-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 474-6300
TELEFRAY. (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acids
                            Query Match 89.2
Best Local Similarity 88.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-475-680-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-475-680-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                         1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                        DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                           1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66, Application US/08714017
; Sequence 66, Application US/08714017
; Patent No. 6040176
; GENERAL INFORMATION:
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                 Length 116;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
                                                                              Score 530.5; DB 2;
Pred. No. 3e-44;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/286,754
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-AUM-1933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-AUW-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-AAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6040176and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IELEFAX: (312) 474-6300
IELEX: 25-3856
INPORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS: LENGTH: 116 amin
                                                                              Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-714-017-66
, MOLECULE TYPE: protein US-08-720-420A-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90909
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1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 DFVMTQTPLSLPVSLGDQASISCRASQSLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPP-TFGGGTKLEIK 271
                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Description of Artificial Sequence: Amino acid; OTHER INFORMATION: sequence for L49-sFV-bL including PelB leader US-09-070-637-20
                            APPLICANT: SIEMERS, NATHAN O.
APPLICANT: SENTER, SUGAN
APPLICANT: SENTER, DEUTER D.
TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS
FILE REFERENCE: 9197F-83.1
CURRENT APPLICATION NUMBER: US/09/070,637A
CURRENT FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: 60/045,888
EARLIER FILING DATE: 1997-05-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 20
LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Process for Generating Specific Antibodies 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%; Score 526; DB 5; Length 218; ilarity 92.0%; Pred. No. 1.6e-43; Conservative 3; Mismatches 4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

88.5%; Score 526.5; DB 3; Length (
Best Local Similarity 89.4%; Pred. No. 4.5e-43;
Matches 101; Conservative 6; Mismatches 5; Indels
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GENERAL INFORMATION:

ATTLE OF INVENTION:

NUMBER OF SEQUENCES: 61

COMPUTER READABLE FORM:

COMPUTER: IEM PC compatible

OPERATING SYSTEM:

COMPUTER: ASCIT (text)

COMPUTER: ASCIT (text)

COMPATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acida
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Best Local Similarity
Matches 104; Conserv
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                                                                    1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLOKPGOSPKLLIHKVSNRF
                                                                                              5 DIVWIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLIYKVSNRP
                              1; Gaps
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                                                                                                                                                                               65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYXCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hackett, Jr., John R.
APPLICANT: Hoff, Jane A.
APPLICANT: Ostrow, David H.
APPLICANT: Golden, Alan M.
TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND TITLE OF INVENTION: COUTROLS
NUMBER OF SQUENCES: 70
CORRESPEDINGES: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STREET: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

89.2%; Score 530.5; DB 3; Length 131;
Best Local Similarity 91.2%; Pred. No. 3.4e-44;
Matches 103; Conservative 4; Mismatches 5; Indels 1
                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,939
88.5%; Pred. No. 3e-44;
ive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICALL.

TELING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REPRENCE/DOCKET NUMBER: 5865.US.01
TELEPHONE: 847-935-1729
TELEPHONE: 847-935-2623
TELEPHONE: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08589939
Patent No. 6015662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: single
Best Local Similarity 88.5
Matches 100; Conservative
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Length 638;

61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113 RESULT 14 US-08-398-613A-48

RESULT 12 US-09-070-637-20 ; Sequence 20, Application US/09070637A ; Patent No. 6132722

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1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLRISRVEAEDLGLYFCSQSTHV-PLTFGAGTKLELK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 88.0%; Score 523.5; DB 1; Length 131; Best Local Similarity 90.3%; Pred. No. 1.6e-43; Matches 102; Conservative 6; Mismatches 4; Indels 1
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              OPERATING SYSTEM: PC-DOS/USS-COCYMERS Withbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-Mar-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 01-Mar-1995
APPLICATION NUMBER: 34,659
ATYONIEX, FACENT INFORMATION:
NAWE: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REPRERENCE/DOCKET NUMBER: 94,659
REPREPREDE/COMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 18, 2005, 10:07:35 Job time : 20 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: Linear
US-08-398-612A-48
                                      94080
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        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
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Patent No. 5686070

GENERAL INFORMATION:
APPLICANT: Docerbuk, Claire M.
APPLICANT: Docerbuk, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SEQUENCE: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: South San Francisco
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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Sequence 48, Application US/08398613A
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Matches 102; Conservative
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US-08-398-612A-48
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immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy; cancer; cell surface glycosphingolipid.
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Adis7084
Adis7084
Adis7088
Aari8758
Aaw90222
Aaw90222
Adk14579
Aaw90223
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                             ADJ57084
ADJ57088
ADJ57088
ADJ57088
ADJ5708022
ADJ50227
ADJ5027
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/label= huVHFR1
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/label= huVHFR2
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  WO2004055056-A1
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Region
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Adg67527 14.18 ant
Aar11597 Murine mo
Aar27851 Mouse 14.
Adg67527 14.18 ant
Aae27841 Mouse 14.
Adg67521 14.18 ant
Aae27849 Mouse 14.
Adg67511 14.18 ant
Aae27849 Mouse 14.
Adg67511 14.18 ant
Aae27845 Mouse 14.
Adg67517 14.18 ant
Adg67517 Antos 14.18 ant
Aae27845 Mouse 14.
Adg67517 Antos ant
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704.902 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                       US-10-737-208A-2
593
1 EVQLVQSGAEVEKPGASVKI.......XYCVSGMEXWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                              April 18, 2005, 09:41:10 ; Search time 62 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2105692
                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2105692 seqs, 386760381 residues
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Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
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ADP42861
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geneseqp1990s:*
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Best Local Similarity

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The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents humanised immunoglobulin heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents an immunoglobulin heavy chain-IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin, variable region, antibody, GD2, cytostatic, gene therapy, cancer, cell surface glycosphingolipid, IL-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New modified m14.18 antibodies with reduced immunogenicity and that specifically bind the human cell surface glycosphingolipid GD2, useful
                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                               EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                                    Length 113;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                      Score 593; DB 8; Pred. No. 2e-45;
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP42961 standard; protein; 575
                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2002; 2002US-0433945P
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERE ) MERCK PATENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-488049/46.
N-PSDB; ADP42959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically bind th
for treating cancer.
                                                                                                                                                                                                                Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein.
                                                                                                                                                                 Sequence 113 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004055056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gillies SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP4296:
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Length

DB 8;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                       Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                                      EVÓLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                         EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMMWVRQNIGKSLEWIGAIDPYYGGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an immunogenically modified fusion protein
                                                                                                                                   61 NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVIVSS 113
                                                                                                                    61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                               Indels
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               Pred. No. 1.1e-44;
Mismatches 0;
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Pred. No. 1.5e-42;
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Way JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 19; Page 78; 92pp; English.
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                                                                                                                                                                                                                                                                                                              Mouse 14.18 antibody VH region #1.
100.0%; Pr.
                                                                                                                                                                                                                         AAE27853 standard; protein; 113
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Baker M,
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05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                                  (first entry)
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                               113; Conservative
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Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERE ) MERCK PATENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113 AA;
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                                                                                                                                                                                                                                                                                  13-DEC-2002
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61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule identified is useful for preparing a biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
                                                                                                                                                                                                                          human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                                                                                                                                                                                            14.18 antibody VH mouse peptide threaded modified epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams S, Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.6%; Score 561; DB 5; L. Best Local Similarity 94.7%; Pred. No. 1.5e-42; Matches 107; Conservative 2; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 21; Page 66; 85pp; English.
                                                                                             ADG67525 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones T,
                                                                                                                                                                                                                                                                                                                                                                                                                        2001EP-00105777.
2001EP-00106536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001EP-00106899.
2001EP-00107012.
2001EP-00107568.
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12-NOV-2001; 2001EP-00126859
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                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to MHC molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-750424/81
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                                                                                                                                                                                                                                                                                                          WO200269232-A2
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20-MAR-2001;
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30-MAY-2001;
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                                                                                                                              ADG67525;
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derlyed from a parent fusion protein, comprising first and second proteins, Polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                            Mouse, fusion protein, immunological, major histocompatability complex; MHC; gastric upset, nausea, 14.18 antibody.
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                     113
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61 NOKFKGRATLTVDKSSSTAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS
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Pred. No. 4.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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Way JC;
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                                                                                                                                                                                                                                                                                                         Mouse 14.18 antibody VH region #2.
                                                                                                                                                  AAE27855 standard; protein; 113
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Baker M,
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                                                                                                                                                                                                                                                        (first entry)
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Watkins J,
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ID ADG6
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chimaeric binding protein; immunoglobulin; variable region; mouse.

119. .132 /label= J(H4) 133. .153 /label= constant region

89US-00409889 89US-00409889

20-SEP-1989; 20-SEP-1989;

WO9104329-A. 04-APR-1991.

label= variable

20. .153

Protein Peptide

Region Region Region

l. .19 /label= leader peptide

Jocation/Qualifiers

fus musculus

Key.

Murine monoclonal 14.18 H chain V region.

(first entry)

14-JUN-1991

AAR11597;

Ą.

AAR11597 standard; protein; 153

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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful tor preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule identified is useful for preparing a biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                  human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
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92.9%; Pred. No. 4.1e-42;
ive 4; Mismatches 4;
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                                                                                                                  14.18 antibody VH mouse modified epitope.
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2001EP-00106538
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30-MAY-2001; 2001EP-00113228
19-OCT-2001; 2001EP-00124855
12-NOV-2001; 2001EP-00126855
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                                                            (first entry)
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Matches 105, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-750424/81
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                                                                                                                                                                                                                                                                                                                                 WO200269232-A2.
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20-MAR-2001; 2
27-MAR-2001; 3
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15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2001;
                                                         11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                              36-SEP-2002
ADG67527;
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Two separate H and L chain cDNA libraries were prepared from mRNA library was enriche hybridoma cell line 14.18. The lambda gt10 library was enriched for full-length L- and H-chains. It was screened by filter hybridiaation using various C region probes. Ten phage clones from each screening were analysed further by restriction analysis. The longest H cDNA sequence was sequenced. It appears to encode a normal length Ig leader peptide. To ensure translation starts from the second ATG codon once additional 5' sequences have been added to the insert, the cDNA is truncated by limited Balll exonuclease treatment. An XhoI linker was then added to give a sequence which, when expressed, will result in an mRNA encoding a normal Ig leader sequence and a functional variable region. The deduced amino acid sequence is given here. See also AAQ11292 9 79 20 EVQLLQSGPELEKPSASVMISCKASGSSFTGYNMMVRQNIGKSLEWIGAIDPYYGGTSY 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY Gaps 61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113 . 0 93.8%; Score 556; DB 2; Length 153; 92.9%; Pred. No. 5.7e-42; ive 4; Mismatches 4; Indels Example, Fig 2; 52pp; English. Matches 105; Conservative Local Similarity Sequence 153 AA; 80 Query Match 셤 ઠે g ð

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Gaps

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113

NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS

19 61

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RESULT 7

1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 

Fusion protein prodn. - e.g. having dual biological activity, esp. antibodies, by transfecting host cell with constructed cassette and second DNA sequence.

WPI; 1991-117518/16. N-PSDB; AAQ11291.

(ABBO ) ABBOTT LAB

Gillies SD;

RESULT 8

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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silicotechniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule identified is useful for preparing a biological activity, where the T-cell epitope is a limer peptide. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
             human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
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88.5%; Pred. No. 2.5e-40;
ive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams S,
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25-APR-2001; 2001EP-00110220
30-MAY-2001; 2001EP-00113228.
19-OCT-2001; 2001EP-00124965.
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2001EP-00106899
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12-NOV-2001; 2001EP-00126859
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20-MAR-2001; 2001EP-00107012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding to MHC molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 113 AA;
                                                                                               WO200269232-A2
                                                                Unidentified
                                                                                                                                                                                                                                                 15-MAR-2001;
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                                                                                                                                         Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                  Williams S;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Hamilton A,
                                                                                                             Mouse 14.18 antibody de-immunised VH5 modified epitope.
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Way JC;
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            AAE27851 standard; protein; 113 AA.
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Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG67523 standard; protein; 113
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05-APR-2001; 2001EP-00108291.
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                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Carr FJ,
Watkins J,
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                                                                                                                                                                                                                              WO200266514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide.
                                                                              13-DEC-2002
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                                                                                                                                                                                                                                                               29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                               Gillies S,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanlon M,
                                           AAE27851;
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Hamilton A;

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Length 113;

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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-potide biological molecule identified is useful for preparing a biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 21; Page 65; 85pp; English.
                                                                                                                                                  08-MAR-2001; 2001EP-00105777.
15-MAR-2001; 2001EP-00106536.
15-MAR-2001; 2001EP-00106538.
20-MAR-2001; 2001EP-00106599.
20-MAR-2001; 2001EP-00107012.
27-MAR-2001; 2001EP-0010768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones T,
                                                                                  18-FEB-2002; 2002WO-EP001688
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tes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 113 AA;
                                          06-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in properties of a composition or in creating new properties of a composition which elicits biological of fracts without having undesirable physiological effects such as nauses of gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
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                                            Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKGRATLSVDKSSSQAYMFLKSLTSEDSAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                              Hamilton A, Williams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.9%; Score 527; DB 5;
87.6%; Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                            Carter G,
Way JC;
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Mouse 14.18 antibody VH modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 19; Page 77; 92pp; English.
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Baker M,
                                                                                                                                                                                                                                                                                          19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
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Best Local Similarity 87.67
Matches 99; Conservative
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                                                                                                                                                         WO200266514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide.
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Hamilton A;

Williams S,

Hanlon M,

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Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
            Mouse 14.18 antibody de-immunised VH4 modified epitope.
                                                                                 Ä.
                                                                              AAE27849 standard; protein; 113
                                                                                                                            (first entry)
                                                                                                                           13-DEC-2002
                                                                                                    AAE27849;
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human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.

WO200269232-A2

Unidentified

14.18 antibody VH veneered modified epitope.

(first entry)

11-MAR-2004

ADG67513;

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Gaps

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us-10-737-208a-2.rag

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Mouse, fusion protein, immunological, major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
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AAE27843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVOLLOSGPELKKPGASVKISCKASGSSFIGYNMNWVRQAPGORTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
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                                                                                                                               Hamilton A, Williams
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86.7%; Pred. No. 3e-39;
iive 7; Mismatches
                                                                                                                             Carter G,
Way JC;
                                                                                                                                                                                                                                               Example 19; Page 78; 92pp; English.
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Baker M,
                                             18-FEB-2002; 2002WO-EP001690.
                                                                   19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291
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08-MAR-2001; 2001EP-00105777.
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                                                                                                                            Carr FJ,
Watkins J,
                                                                                                                                                                WPI; 2002-667054/71
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es 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113 AA;
WO200266514-A2
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                                                                                                                                                                                                                          polypeptide.
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                                                                                                                                        Hanlon M,
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(first entry)

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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (HGC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically nonmodified biological molecule identified is useful for preparing a modified biological extivity, where the T-cell epitope desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                          Hamilton A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 21; Page 66; 85pp; English
15-MAR-2001; 2001EP-00106538.
20-MAR-2001; 2001EP-00106699.
20-MAR-2001; 2001EP-00107012.
27-MAR-2001; 2001EP-00107568.
25-MAR-2001; 2001EP-00110220.
30-MAY-2001; 2001EP-0011328.
19-CTT-2001; 2001EP-00114965.
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Best Local Similarity
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Job time : 64 secs
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                                                                                                                                                                                                                                The invention relates to an immunogenically modified fusion protein
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                                                            Williams S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified fusion protein with reduced immunogenicity, useful
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                                                                                                                                              combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                  87.9%; Score 521; DB 5; Length 113;
85.8%; Pred. No. 5.5e-39;
Live 7; Mismatches 9; Indels
                                                            Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.18 antibody de-immunised VH1 modified epitope.
                                                          Carter G,
Way JC;
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                                                          Jones T, Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001EP-00105777.
2001EP-00106536.
2001EP-00106538.
05-APR-2001; 2001EP-00108291
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2001EP-00107012.
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25-APR-2001; 2001EP-00110220.
30-MAY-2001; 2001EP-00113228.
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                           (MERE ) MERCK PATENT GMBH.
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                                                          Carr FJ,
Watkins J,
                                                                                                   WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200269232-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2001;
08-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2001;
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                                                                         Hanlon M,
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                                                         Gillies
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The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (WHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful to preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule definition is useful for preparing a modified biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
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0
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85.8%; Pred. No. 5.5e-39;
ive 7; Mismatches 9; Indels
                                                                                                               Hamilton A;
                                                                                                            Williams S,
                                                                                                                                                                                                                                                                                                        Example 21; Page 66; 85pp; English.
                                                                                                                 ,
19-OCT-2001; 2001EP-00124965.
12-NOV-2001; 2001EP-00126859.
                                                                                                                 Jones
                                                                 (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 85.8
                                                                                                            Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113 AA;
                                                                                                            Carr FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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Search completed: April 18, 2005, 10:00:58

9 9

1 BVQLLQSGPELKKPGASVKISCKASGSSFTGYNWNWRQAIGQRLEWIGLIDPYYGGTSY

NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

April 18, 2005, 09:57:11; Search time 11.5 Seconds (without alignments) 945.434 Million cell updates/sec Run on:

Title: Perfect score:

US-10-737-208A-2 593 1 EVQLVQSGAEVEKPGASVKI......YYCVSGMEYWGQGTSVTVSS 113 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database :

'PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Iq heavy chain pre	heavy chain v	ti-DNA	heavy	Ig heavy chain V r	Ig heavy chain V-D		Ig heavy chain pre	heavy chain	i-glycoprote	Ig heavy chain pre	neavy chain	neavy chain V	neavy chain V	neavy	neavy		neavy chain	neavy chain V		heavy chain V	heavy		-		-	b	heavy	
SUMMARIES	Ω	H32513	F30502	PL0200	PL0084	PN0444	809957	S26319	A27609	PS0057	E45722	PL0011	MHMS38	137267	836265	PH0099	MHMS4E	T01407	MHMSJS	S41394	849530	S55542	B53285	PH0100	A32483	F45722	PH0971	JL0077	PH0961	PH0105
	h DB	7 2		8							•				•		7			7									•	
	Length	137	119	118	11	15	11	11	13	13	12	15	11	12	11	11	11	14	11	12	13	11	11	12	14	12	10	13	11	13
de	Query	79.5	78.8	77.4	74.5	74.3	72.1	71:9	71.9	71.8	71.6	71.5	71.4	9.07	70.4	70.2	69.8	69.8	69.5	69.2	69.5	69.0	69.0	69.0	69.0	68.9	68.8	68.5	68.5	68.5
	Score	471.5		459	41.	440.5	427.5	426.5	426.5	425.5	424.5	424	423.5	418.5	417.5	416	414	414	412	410.5	410.5	409	409	409	409	408.5	408	406.5	406	0
	Result No.	-		6	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

Ig heavy chain V r	heavy chain	pelB leader/Ig hea	heavy chain	heavy chain	chain	Ig heavy chain V-1	Ig heavy chain pre	Ig heavy chain V-1	Ig mu chain precur	Ig heavy chain V r	Iq heavy chain pre				
PH0962	A49982	PH0958	PH0887	C37267	MHMS18	PC4402	PH0952	866537	PH0960	A33548	S04575	C33548	S14683	PH0954	PS0024
~	7	~	~	~	-	4	~	~	~	~	7	7	~	~	~
120	120	122	122	128	139	287	128	131	136	129	140	133	627	132	139
68.4	68.2	68.2	68.2	68.0	67.9	67.9	67.7	67.7	67.7	67.6	67.6	67.5	67.5	67.4	67.4
	4.5	04.5	104.5	403.5	402.5	402.5	401.5	401.5	401.5	401	401	400	400	399.5	399.5
405.5	40,	4	ν.												

## ALIGNMENTS

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19 heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J.Cin. Invest. 82, 862-860, 1888
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:313826
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <kOF>
A;Cross-references: GB:MO1811; NID:g196849; PIDN:AAA38848.1; PID:g196950
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
RESULT 1
H32513
```

1; Gaps 2 Length 137; 12; Indels DB 2; 79.5%; Score 471.5; DB 2 76.3%; Pred. No. 6.3e-36; tive 11; Mismatches 12 Query Match Best Local Similarity 76.3% Matches 90; Conservative

9 20 BIQLQQSGAELVKPGASVKISCKASGYSFTGYNMWWKQSHGKSLEWIGNINPYYGSTSY 79 1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMIWVRQNIGKSLEWIGAIDPYYGGTSY a ઠે

61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCV----SGMBYWGQGTSVTVSS 113 ò g

F30504C
Is house mouse)
C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Accession: F30502
R, Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A, Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mis.
A, Reference number: A30502, MUID:88315787; PMID:2457627
A, Accession: F30502
A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-119 < EILC, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < INM>

Gaps 7; Length 119; Indels Query Match 78.8%; Score 467.5; DB 2; Best Local Similarity 74.8%; Pred. No. 1.3e-35; Matches 89; Conservative 11; Mismatches 12;

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1;

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Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0444
R;Kaluua, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A;Reference number: PN0444; MUID:93138402; PMID:1339379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V-D-J region (106-10E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accesion: 809957
R;Reininger, L; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Bur, J. Immunol. 20, 71-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie:
A;Reference number: 809955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EVQLQQFGABLVKPGTSVKISCKASGYIFTDYNMDWVKQSHGKSLEWIGDIDPNFDSSSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
             61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 NQKFKGKATLIVDKSSNTAYMELRSLISEDTAVYYCARGGFPYGMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: PN0444
A,Molecule type: mRNA
A,Gross-references: GS1-L02346
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <AGT>
F;20-150/Product: Ig heavy chain V region #status predicted <MAT>
F;20-117/Domain: variable region <VRG>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 150;
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A; Residues: 1-112 < REI.
A; Cross-references: EMBL:X51845; NID:g55244; PIDN:CAA36138.1; P:
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Best Local Similarity 72.9%; Pred. No. 4.5e-33;
Matches 86; Conservative 11; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.1%; Score 427.5; DB Best Local Similarity 73.5%; Pred. No. 5e-32; Matches 83; Conservative 12; Mismatches 1
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Cispecies: Was musculus (house mouse)
Cibate: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
CiAccession: PLO089
R.Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A.Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are
A.Reference number: PLO080; MUID:89094248; PMID:2492056
A.Reference number: PLO080; MUID:89094248; PMID:2492056
A.Residues: 1-118 <AMES
A.Residues: 1-118 <AMES
A.Residues: GB.XB8595; GB:Y00794; NID:951573; PIDN:CAA41470.1; PID:9938254
A.Rosersences: GB.XB8595; GB:Y00794; NID:951573; PIDN:CAA41470.1; PID:9938254
A.Note: 66-GJV is translated as """ from the vergion of an antidiotypic monoclonal ant C; Superfamily: immunoglobulin V region; immunoglobulin homology
CiReywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                    C. Accession: PL0200
R. Smith, R.G.; Vose Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A.Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from NA-Natesence number: PL0198; MUD:90309768; PMID:2114528
A. Accession: PL0200
A. Molecule type: mRNA
A. Residues: 1-118 «SMI»
A. Cross-references: GB: X53641; NID:g50193; PIDN: CAA37692.1; PID:g930139
C. Superfamily: immunoglobulin homology «Immunoglobulin homology F. 15-98 Domain: immunoglobulin homology «Immunoglobulin homology »
F. 30-106 Region: complementarity-determining 3
F. 50-106 Region: complementarity-determining 3
F. 99-106 Region: Transity determining 3
F. 99-106 Region: Transity determining 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment) Species: Mus musculus (house mouse) Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J heavy chain V region (E4) - mouse
Species: Mus musculus (house mouse)
Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
      EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                    1 EVQLQQSXXELEKPGASVKISCKASGYSFIGYSMNWVKQSNGEXLEWIGNIDXYLGGTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.4%; Score 459; DB 2;
74.6%; Pred. No. 7.3e-35;
tive 10; Mismatches 12
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Best Local Similarity 74.6*
Matches 88; Conservative
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A, Accession: PS0057
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-135 < VAO>
A, Conser-references: GB:D00307; NID:g220448; PIDN:BAA00213.1; PID:g220449
A, Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly, A, Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly, Superfamily: immunoglobulin to region; immunoglobulin homology
C, Superfamily: immunoglobulin
F;1-19/Domain: signal sequence #status predicted < SIG>
F;0-15/Product: Ig heavy chain V region PAR #status predicted < MAT>
F;34-117/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (fr. Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cibate: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
Ciscession: E45722
Risimpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vaseq. J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on his A;Reference number: A45722; MUID:93100833; PMID:7677958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-151 cCHE>
A,Experimental source: cell line 4C11
C,Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 YNQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS-----GMEYWGQGTSVTVSS 113
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: Ph0011
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
MO1. Immunol, 25, 33-40, 1988
A;Fitle: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 EVQLQQSGPELVKPGASVKISCKASGYSFTGYFMWVKQSHGKSLEWIGRINPYNGDTFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRONIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 NQKFKGKATLTVDKSSSTAHMELRSLTSEDSAVYYCARLNYRGAYWGQCTLVTVSA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 135;
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        A; Reference number: PS0057; MUID:89197817; PMID:2467902
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Pred. No. 1e-31;
Tricheg 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 425.5; DB 2
Pred. No. 9.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
71.8%; Score 425.5; I
Best Local Similarity 73.3%; Pred. No. 9.3e-
Matches 85; Conservative 10; Mismatches
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Best Local Similarity
Matches 85; Conserv
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C;Species: Mus musculus (house mouse)
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: 1.29 lymphoma cells express a nonmutated V-H gene before and after H chain swit A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <a href="https://docs.org/links/region/">kirlin: A27609</a>
A;Molecule type: DNA
A;Residues: 1-139 <a href="https://docs.org/links/region/">kirlin: A27609</a>
A;Molecule type: DNA
A;Residues: 1-139 <a href="https://docs.org/links/region/">kirlin: A27609</a>
A;Coss-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
C;Generican: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;10-19/Domain: signal sequence #status predicted <NAR>
F;34-117/Domain: immunoglobulin homology <IMM>
F;34-117/Domain: immunoglobulin homology <IMM>
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R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
                                                                                                                                                                                                                                    a protein
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                                                                                            C: Accession: $26319
R:Stark S.E.; Caton, A.J.
T. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in A: Reference number: $26309; MUID:91341421; PMID:1908510
A: Reference number: $26309; MUID:91341421; PMID:1908510
A: Reseason: $26319
A: Residues: 1-114 <STA>
A: Residues: 1-114 <STA>
A: Residues: 1-114 <STA>
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Reywords: heterotetramer; immunoglobulin P: Immunoglobulin P: Immunoglobulin P: Immunoglobulin C: Reywords: immunoglobulin homology <Immunoglobulin homology <Immunoglobulin P: Immunoglobulin 
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Ig heavy chain precursor V region (PAR) - mouse
C;Species: Mus musculus (house mouse)
C;Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
                            C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSGPELVKPGASVKISCKASGYSFTGYFMWWVKQSHGKSLEWIGRINPYNGDTFYNQKFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 426.5; DB 2
Pred. No. 6.3e-32;
9; Mismatches 15
heavy chain V region - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.9%;
ilarity 74.3%;
Conservative
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Best Local Similarity
Matches 84; Conserv
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les 85; Conserv
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Best Local S
Matches 85
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C;Keywords: heterotetramer; immunoglobulin F;19-102/Domain: immunoglobulin homology <IMM>
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                                                                                                                                             70.6%;
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                                                                                                                              Query Match
Best Local Similarity 66.7*
Matches 82; Conservative
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nes 83; Conservative
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R) Didrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984
A;Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
A;Reference number: A91000; MUID:84182519; PMID:6201362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J heavy chain V region (AC38 205.12) - mouse
Species: Mus musculus (house mouse)
Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin (5.Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <81G>F;20-136/Product: IG heavy Chain V region 4C11 #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <1PM>F;34-117/Domain: immunoglobulin homology <1PM>F;36-88/Region: complementarity-determining 1 F;69-88/Region: complementarity-determining 2 F;118-125/Region: complementarity-determining 3 F;118-125/Region: C region (fragment) #status predicted <COR>
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                                                                                                                                                                                                                                                                                                                                                                                   Ch 71.5%; Score 424; DB 2; Length 151; I Similarity 70.1%; Pred. No. 1.46-31; B2; Conservative 13; Mismacches 18; Indels 82; Conservative 13; Mismacches 18; Indels
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A;Molecule type: protein
A;Residues: 1-118 <DIL.3
A;Cross-references: UNIPROT:P06330
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
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Best Local Similarity 71.2%; Pred. No. 1.2e-31;
Matches 84; Conservative 10; Mismatches 19
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F;22-96/Disulfide bonds: #status predicted
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Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 115-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C;Accession: PH0099
R;Schmitter, D; Poch, O; Zeder, G; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V, A.D. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S36265
R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Byed. J. 12, 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries. A; Reference number: S36256; MUID:93178448; PMID:7679990
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                 6 VQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGGTSYN
                                                                                                                                                                                                                                                                                  62 OKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG-------MEYWGQGTSVT
                                                                                                                                         2 VQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSYN
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                                                                             Gaps
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A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:G33121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                      Indels 11;
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       Length 128;
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A; Residues: 1-119 <SCH>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
E; 15-98 | Domain: immunoglobulin homology < IMM>
F; 15-98 | Domain: immunoglobulin homology < IMM>
F; 13-35 | Region: complementarity-determining 1
F; 50-66 | Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%; Score 417.5; DB 2; 70.3%; Pred. No. 4.3e-31; iive 14; Mismatches 16;
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; Score 418.5; DB ; Pred. No. 3.8e-31 13; Mismatches 1
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DB 2; Length 119;

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Best Local Similarity 70.1%; Pred. No. 5.9e-31; Matches 82; Conservative 13; Mismatches 18; Indels 4; Gaps 1;
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1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMAWVRQNIGKSLEWIGAIDPYYGGTSY	9	9
	1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY	 1 EVQLQQSGPELVEPGASMKISCKASGYSFAGYTMIWVKQSHGKNLEWIGLINPYDGSIAT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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HSRBL, AR207936, AAL09420.1; -.
HSSP; P01751; 1NQB.
SMART, SM00406; IGV; 1.
NON TER 10 10
NON TER 12 120
SEQÜENCE 120 AA; 13204 MM; DC4834ABIDE56F3C CRC64;
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                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                              120 AA
                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                    Q924P6
HV11 MOUSE
Q96QS0
                                                                                                                                                                                                                                                                                                                          Created)
             Q924P5
Q924P9
Q8K0F2
Q924R7
Q9D8L4
Q6PJB2
Q924Q2
Q91VA2
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
 [1] =
SEQUENCE FROM N.A.
STRAIN=C3H/HeJ-lpr;
                                                                                                                                                                                                                                                                                                                                                                             (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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 01-DEC-2001
01-DEC-2001
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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                           Q920E8;
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1920B8
10 0920B8
10 0920B
DT 01-D1
DT 0
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homo sapien
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684.792 Million cell updates/sec
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593
1 EVQLVQSGABVEKPGASVKI......YYCVSGMEYWGQGTSVTVSS
                                                                                             April 18, 2005, 09:42:15 ; Search time 84.5 Seconds
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099xe9
099xe9
094xf0
091mkl
091mkl
091mkl
092kl72
0924kl
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8VIJ1
Q9QXE9
HV51 MOUSE
Q9QXF0
Q65ZR6
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091WR1

0924R0

0924R1

0924R1

0924R1

0924R1

0924R1

0924R2

0924R2

0924R2

0924R2

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Q924Q7
Q924R5
Q924Q4
Q924Q8
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot sprot:*
2: uniprot trembl:*
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Maximum DB seq length: 200000000
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Match Length
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11145
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1470
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                                                                    OM protein
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1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMMYKQSHGKSLEWIGDINPNNGGTSY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEY-----WGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFKGKATLIYDKSSSATYMELRSLTSEDSAVYYCARGYGYDFDVWGTGTTVTVSS 118
                                                                                                                                                                                                                                                                                                                                               Diddrop R., Bovens J., Sievettz M., Beyreuther K., Rajewsky K.;
Diddrop R., Bovens J., Sievettz M., Beyreuther K., Rajewsky K.;
A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523[194].
EMBO J. 3:517-523[194].
EMBO J. 3:517-523[194].
InterPro JPR007101 Ig-like.
InterPro JPR007101 Ig-like.
InterPro JPR00710 Ig-like.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
Direct protein sequencing; Immunoglobulin V region.

V segment.
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 423.5; DB 1; Length 118; 71.2%; Pred. No. 7.1e-36; ive 10; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemens A., Rademaekers A., Specht C., Koelsch B.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ25171; CAB65236.1; -.
R PIR; PH0973; PH0973.
R HSSP; P01751; INQB.
R InterPro: IPR007110; Ig-like.
R InterPro: IPR00710; Ig-like.
R SMART; SM00406; IGV; I.
R ROSITE; PS50835; IG_LIKE; 1.
R NON TER 17 17
SEQÜENCE 117 AA; 13060 MW; DB16AD0858A47E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 104 D segment.
105 118 J segment.
2 96 By similarity.
118 118 AN; 12934 MW; 94F7BEB4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 117
117 AA; 13060 MW; D816AD0858A47E4C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.3%; Score 423; DB 2; 70.9%; Pred. No. 8e-36;
                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g heavy chain V region AC38 205.12.
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D segment.
J segment.
By similarity.
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                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE
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Q9QXF0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                    Wioch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.; "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from CJH-DPr mice and lupus mice with nephritis."; But. J. Immunol. 26:2225-233(1996).

EMBL, VISSI4, AAB02916.1; SHORT; SNO0406; INOB.

SWART; SNO0406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mush.TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.5%; Score 436; DB 2; Length 123; Best Local Similarity 68.3%; Pred. No. 3.8e-37; Matches 84; Conservative 11; Mismatches 18; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ222174; CAB65237.1; -.
PIR; F33932; P33932.
INCEPP: INOB.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SM00406; IGV; 1.
PROSITE; PSE0835; IG_LIKE; 1.
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123 AA; 13806 MW; CC0037A806E9911E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1mmunoglobulin heavy chain V-D-J region (Fragment).
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Best Local Similarity 73.5%; Pred. No. 4.6e-
Matches 86; Conservative 10; Mismatches
MEDLINE=96409289; PubMed=8814271;
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HV51_MOUSE
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SEQUENCE
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Q9QXE9

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STANDARD;

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Gaps

Matches

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY
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STRAIN=FVB/N; TISSUE=Kidney;
MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO55910; AAH55910.1; -.
HSSP; P01865; 1KBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003506; Ig_WHC.
Interpro; IPR003506; Ig_v.
Pfam; PR07654; C1-set; 3.
SWART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 4.
PR0SITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2e-34;
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12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CZECH II; TISSUE-Mammary tumor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Conservative
                                                                                                                                                                                                                                                                                                                                                cDNA sequences.
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                                                                                                                         61 NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG----MEYWGQGTSVTVSS 113
                                                                                                                                                  61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG----MEYWGQGTSVTVSS 113
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
"Junctional diversity of H and L chains allows the coexpression of wutually exclusive idiotopes (Idilo4 and IdiS58).";
J. Immunol. 146:4024-4030(1991).
EMBL: M7413P, AAA7776.1;
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein A1324046.

Name-A1324046;
Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae.
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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    18; Indels
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Last annotation update)
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    12; Mismatches
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                                                                                                                                                                                                                                                                                                                        Created)
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  83; Conservative
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NCBI_TaxID=10090;
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Best Local Simil
Matches 82, C
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodiigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
A. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A. Jones S.J., Marra M.A.;
T. and mouse cDNA sequences.";
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Biochemistry 21:5415-5424 (1982)
-!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma protein has also been determined.
-!- MISCELLANEOUS: This protein binds dextran.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02039; MHMS4E.
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-1986 (Rel. 44, Last amnotation update)
IG heavy chain V region MOPC 104E.
Buka musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; MusillaraxID=10090;
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MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 488;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013339, AAH1339.1; -.
HSSP; P01751; 1A6W.
MGD; MGI:96486; Igh-VJ558.
Pfam; PF07654; C1-set; 2.
SMART; SMO0406; IGV; 1.
PROSITE; PS00290; IGV; 1.
PROSITE; PS00290; IGMHC; UNKNOWN 2.
SEQUENCE 488 AA; 52964 MW; F12068460B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Best Local Similarity 65.3%; Pred. No. ....
Watches 81; Conservative 14; Mismatches
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STRAIN=FVB/N; TISSUE=Kidney;
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CARAINEMENT FORNIN, TISSUE=Mammary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

Ratausherg R.L., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Joedan H., Moore T., Max S.L., Wang J., Haishe F.,

Altschul S.F., Joedan H., Moore T., Max S.L., Wang J., Haishe F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bromstein M.J., Ugdin T.B., Toshiyuki S., Carninol P., Prange C.,

Raha S.L., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Touchman J.W., Green E.D., Dickson M.C.,

Radiquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYCARDYDWYFDVWGAGTTVTVSS 117
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                Glycoprotein; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                  Ig-like.
By similarity.
N-linked (GlCNAc. . .) (complex)
                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-mix FVB/N; TISSUE-Mammary tumor; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; F33932; F33932.
PIR; F31932; F33932.
PIR; PH1105; PH1105.
PIR; PH1108; PH1106.
                                                                                                                                                                                           1 116 Ig-like.
22 96 By similarity.
55 55 N-linked (GlCNAc. . .) (co
117 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                              Score 414; DB 1;
Pred. No. 6.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Gl DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                          69.88;
InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
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SEQUENCE.

MEDLINE=80078170; PubMed=6765983;

MEDLINE=80078170; PubMed=6765983;

Schilling J., Clevinger B., Davie J.M., Hood L.;

Rair arrangements in heavy chain V-region gene segments.";

Nature 28:135-40(1980).

Lin MiscELLANEOUS: The sequences of 10 hybridoma proteins that also bind dextran differ from that shown at 1-7 positions, many of which occur in the D and J segments.

C. !- MISCELLANEOUS: This protein binds dextran.

MISCELLANEOUS: This protein binds dextran.

PIR; A26242; MHMSJ5.

RSSP, P0173; ANOB.

RICETPO: IPRO0110; Ig-like.

InterPro: IPRO0147; 19; 1.

RR SMART; SM00406; IGV: I.

RR SMART; SM00406; IGV: I.

RR PROSITE; PS50835; IG_LIKE; 1.

RESIDENCE protein sequencing; Immunoglobulin V region.

DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG----MEYWGQGTSVTVSS 113
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                            69.6%; Score 412.5; DB 2; Length 143; 67.8%; Pred. No. 1.2e-34; ive 12; Mismatches 21; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.5%; Score 412; DB 1; Length 117; 70.1%; Pred. No. 1.1e-34;
                                                                                                                                                                                                                                                                                                                             143 AA; 15868 MW; 139B2E966B81E07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-2004 (Rel. 44, Last annotation update)
15-JUL-2004 (Rel. 44, Last annotation update)
Mus musculus (Mouse)
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By similarity.
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                                                                                                         PIR, PH1151, PH1151.
PIR, PH1152, PH1152.
PIR, PH1153, PH1153.
HSSP, PO1751, 1A6W.
SMART, SM00406, IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 67.89
Matches 80; Conservative
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P01757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCV----SGMEYWGOGTSVIVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6;
Kozono Y., Kozono H., Azuma T.;
Submitted (40G-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067790; BAB63275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR00359; Ig_c1.
InterPro; IPR003596; Ig_wHC.
InterPro; IPR0035566; Ig_v.
Pfam; PF07654; C1-8et; Z.
SMART; SM00406; IGv; 1.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG_MC; UNKNOWN 2.
SRQUENCE 482 AA; $\overline{5}2121 MW; A0\overline{6}FF083E771D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0924RO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 69.7%; Score 413.5; DB 2;
1. Similarity 67.8%; Pred. No. 3.7e-34;
80; Conservative 12; Mismatches 21;
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PH1153.
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PH1105.
PH1108.
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PH1142.
PH1149.
PH1150.
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PH1118.
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PH1126.
PH1128.
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PH1129.
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PIR, PH1118; PIR, PH1119; PIR, PH1126; PIR, PH1126; PIR, PH1128; PIR, PH1131; PIR, PH1131; PIR, PH1142; PIR, PH1150; PIR, PH1150; PIR, PH1151; PIR, 
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Mus musculus (Mouse)
                                                  SEQUENCE FROM N.A.
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                                                         STRAIN=C57BL/6;
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HSSP; P01751; 1
SMART; SM00406;
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PH1147;
PH1149;
PH1150;
PH1151;
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PH1142;
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                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                       1,
                                                                                                                                                                                                                                                                                                                                                         'Match 69.4%; Score 411.5; DB 2; Length 145; Local Similarity 66.7%; Pred. No. 1.6e-34; les 80; Conservative 12; Mismatches 21; Indels 7;
                                                                                                                                   Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067794; BAB63279.1; -
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16011 MW; 9BC0846D40DF97EA CRC64;
                                                             Last sequence update)
Last annotation update)
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
V4186.2-D-J-C mu protein (Fragment).
Name=VH186.2-D-J-C mu)
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PROSITE; PS50835; IG LIKE; 1.
                                        PRELIMINARY;
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PH1108.
PH1114.
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PIR; F33932; F33932
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STRAIN=C57BL/6;
                                                                                                         NCBI_TaxID=10090;
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PH1108;
PH1114;
PH1118;
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PH1128;
PH1129;
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01-DEC-2001
01-DEC-2001
01-OCT-2003
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                                   Mus musculus (Mouse).

Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                Kozono Y., Kozono H., Azuma T.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067791; BAB63276.1; -.
PIR; F28833; F33932; F33932.
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STRAIN=CS7BL/6;
Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
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VH186.2-D-J-C mu protein (Fragment).
Name=VH186.2-D-J-C mu;
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PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1 1
NON_TER 145 145
SEQUENCE 145 AA; 16001 MW;
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EMBL; AB067789; BAB63274.1;

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1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
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                              R PIR, F33932; F3393.

R PIR, F33932; F3393.

R PIR, F33932; F3393.

R PIR, P1106; PH1106.

R PIR, PH1106; PH1106.

R PIR, PH1110; PH1114.

R PIR, PH1126; PH1126.

R PIR, PH1129; PH1126.

R PIR, PH1139; PH1139.

R PIR, PH1139; PH1131.

R PIR, PH1139; PH1131.

R PIR, PH1139; PH1131.

R PIR, PH1141.

R PIR, PH1141.

R PIR, PH1141.

R PIR, PH1151; PH1141.

R PIR, PH1151; PH1151.

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R PIR, PH1154.

R PIR, PH155.

R PIR, PH155.

R PIR, PH155.

R PIR, PH156.

R PIR, PIR, PH156.

R PIR, PH156.

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Search completed: April 18, 2005, 10:03:56 Job time : 85.5 secs

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536.541 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMARIES		
Result No.	Score	% Query Match	% Query Match Length D	DB	ΩI	Description	
-	561	94.6	113	15	US-10-468-370-686	Sequence 686, App	
7	561	94.6	113	16	US-10-468-496-2017	Sequence 2017, Ap	
ო	929	93.8	113	15	US-10-468-370-688	688,	
4	556	93.8	113	16	US-10-468-496-2019	2019,	
ស	536	90.4	113	15	US-10-468-370-684	684,	
Q	536	90.4	113	16	US-10-468-496-2015	Sequence 2015, Ap	
7	527	88.9	113	15	US-10-468-370-674	674,	
80	527	88.9	113	16	US-10-468-496-2005	2005,	
σ	524	88.4	113	15	US-10-468-370-682	682,	
10	524	88.4	113	16	US-10-468-496-2013	2013,	
11	521	87.9	113	15	US-10-468-370-676	676,	
12	521	87.9	113	16	US-10-468-496-2007	Seguence 2007, Ap	
13	520	87.7	113	15	US-10-468-370-680	Sequence 680, App	

Sequence 2011, App Sequence 678, App Sequence 13, Appl Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 113, Appli Sequence 154, Appli Sequence 16, Ap	544
16 US-10-468-496-2011 15 US-10-468-496-2011 16 US-10-468-496-2019 11 US-10-207-655-13 12 US-10-642-120-2 16 US-10-642-120-2 16 US-10-642-120-2 16 US-10-642-120-2 16 US-10-642-120-2 17 US-10-642-116-2 18 US-10-642-116-2 19 US-10-642-100-2 17 US-10-642-100-2 18 US-10-642-100-2 19 US-10-642-100-2 17 US-10-642-100-2 18 US-10-642-100-2 19 US-10-642-100-2 15 US-10-642-100-3 15 US-10-10-20-369-10-3 15 US-10-462-062-154 15 US-10-462-062-154 15 US-10-693-10-21-8 16 US-10-389-10-21-8 16 US-10-389-11-6 17 US-10-389-11-6 18 US-10-389-11-6 18 US-10-389-11-6 18 US-10-389-11-6 18 US-10-389-11-6	US-10-45 US-09-21 US-10-76
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## ALIGNMENTS

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US-10-468-370-686

Sequence 686, Application US/10468370

Publication No. US20040082039A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Carr, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Carrer, Graham
APPLICANT: Hanlon, Anita
APPLICANT: Hanlon, Marian
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Watthey, John
APPLICANT: Matthey, John
APPLICANT: Matthey, John
APPLICANT: Matthey
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APPLICANT: Watthey
APPLICANT: Baker, Matthey
APPLICANT: Watthey
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APPLICANT: Baker, Matthey
APPLICANT: Watthey
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Sequence 2017, Application US/10468496

Publication No. US20040180386A1

GENERAL INFORMATION:

APPLICANT: Carter, Graham

APPLICANT: Carter, Graham

APPLICANT: Carter, Graham

APPLICANT: Williams, Stephen

APPLICANT: WINDERTION: INMUNCENCITY

FILE REFERENCE: MER-117

CURRENT APPLICATION NUMBER: 01105954.2

PRIOR FILING DATE: 2001-02-19

PRIOR FILING DATE: 2001-02-19

PRIOR FILING DATE: 2001-03-15

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR FILING DATE: 2001-03-16

PRIOR PRIOR FILING DATE: 2001-03-16

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Query Match
94.6%; Score 561; DB 15; Length 113;
Best Local Similarity 94.7%; Pred. No. 3.2e-44;
Matches 107; Conservative 2; Mismatches 4; Indels
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RESULT 3
US-10-466-370-688
Sequence 688, Application US/10468370
; Publication No. US20040082039A1
; CENERAL INFORMATION:
; APPLICANT: Gilles, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Carr, Gilles, J.
; APPLICANT: Carrer, Graham

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APPLICANT: JOHN SEPLICANT: APPLICANT: JOHN SEPLICANT: JOHN SEPLICANT: JOHN SEPLICANT: JOHN SEPLICANT: APPLICANT: Hamilton, Anita APPLICANT: Hamilton, Anita TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL TITLE OF INVENTION: IMMUNOGENCITY
TITLE OF INVENTION: IMMUNOGENCITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: 2003-03-25
PRIOR FILING DATE: 2001-03-18
PRIOR PELING DATE: 2001-03-18
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-15
PRIOR FILING DATE: 2001-03-20
PRIOR PRIOR PRIOR DATE: 2001-03-20
PRIOR DATE: 2001-03-20
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93.8%; Score 556; DB 15; Length 113;
Best Local Similarity 92.9%; Pred. No. 9.2e-44;
Matches 105; Conservative 4; Mismatches 4; Indels
APPLICANT: Mathems, vorteron, APPLICANT: Matkins, John
APPLICANT: Watkins, John
APPLICANT: Baker: Matthew
APPLICANT: Baker: Matthew
APPLICANT: Way, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REPERENCE: MATLIS
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT PILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 688
LENGTH: 113
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Publication No. US20040180386A1
GENERAL INFORMATION:
APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Unes, Tim
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ORGANISM: Artificial Sequence
FEATURE:
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US-10-468-370-688
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APPLICANT:
APPLICANT:
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                                                                                                                                            Gaps
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                                                                               Query Match

93.8%; Score 556; DB 16; Length 113;
Best Local Similarity 92.9%; Pred. No. 9.2e-44;
Matches 105; Conservative 4; Mismatches 4; Indels
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APPLICANT: Garr, Francis J.
APPLICANT: Garr, Francis J.
APPLICANT: Garr, Francis J.
APPLICANT: Garre, Tenacis J.
APPLICANT: Garre, Tenacis J.
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Martian
APPLICANT: Hanlon, Martian
APPLICANT: Hay, John
APPLICANT: Hay, John
APPLICANT: Hay, John
APPLICANT: Markins, John
TITLE OF INVENTION: IMMUNOGENICITY
FILE OF INVENTION NUMBER: EP 01103955.9
FRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01103291.4
FRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR PILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

90.4%; Score 536; DB 15;
Best Local Similarity 88.5%; Pred. No. 6.4e-42;
Matches 100; Conservative 7; Mismatches 6;
; OTHER INFORMATION: MHC class II binding epitope US-10-468-496-2019
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Sequence 2015, Application US/10468496
Publication No. US20040180386A1
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Publication No. US20040082039A1
GENERAL INFORMATION:
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APPLICANT: Carr, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
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APPLICANT: Hamilton, Anita

TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: IMMUNOGENCITY
FILE REFERENCE: MER-117
FURRENT APPLICATION NUMBER: U310/468,496
CURRENT APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 01105777.5
PRIOR PRILING DATE: 2001-03-08
PRIOR PRILING DATE: 2001-03-15
PRIOR PRILING DATE: 2001-03-15
PRIOR PELING DATE: 2001-03-15
PRIOR PELING DATE: 2001-03-15
PRIOR PELING DATE: 2001-03-15
PRIOR PELING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
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APPLICANT: Baker, Matthew
APPLICANT: Way, Jeffrey
JAPLICANT: Way, Jeffrey
ITLE OF INVENTION: ATTIFICIAL PROTEINS WITH REDUCED
ITLE OF INVENTION: ATTIFICIAL PROTEINS WITH REDUCED
ITLE OF INVENTION: ATTIFICATION
FILE REFERENCE: WER-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR APPLICATION NUMBER: EP 01103291.4
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2002-02-18
PRIOR FILING DATE: 2002-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.4%; Score 536; DB 16; Best Local Similarity 88.5%; Pred. No. 6.4e-42; Matches 100; Conservative 7; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: WHC class II binding epitope US-10-468-496-2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 674
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Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Carr, Francis J.
APPLICANT: Jones, Tim
APPLICANT: Carter, Graham
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Williams, Stephen
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US20040082039A1

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APPLICANT: Carre, Graham
APPLICANT: Carre, Graham
APPLICANT: Jones, Tim
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: IMMUNOGENCITY
FILE REFERENCE: MER-117
FURENT FILING DATE: 2003-09-25
FRIOR PELICATION NUMBER: 01103954.2
FRIOR PELICATION NUMBER: 0110577.5
FRIOR PELICATION NUMBER: 0110577.5
FRIOR FILING DATE: 2001-03-19
FRIOR FILING DATE: 2001-03-15
FRIOR PELICATION NUMBER: 01106538.4
FRIOR FILING DATE: 2001-03-15
FRIOR PELICATION NUMBER: 01106536.4
FRIOR PELICATION NUMBER: 01106536.4
FRIOR PELICATION NUMBER: 0110699.6
FRIOR PELING DATE: 2001-03-20
FRIOR PELING DATE: 2001-03-00
FRIOR PELING DATE: 2
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88.9%; Score 527; DB 16;
Best Local Similarity 87.6%; Pred. No. 4.3e-41;
Matches 99; Conservative 8; Mismatches 6;
                                                                                                                                                                                      Query Match

88.9%; Score 527; DB 15;
Best Local Similarity 87.6%; Pred. No. 4.3e-41;
Matches 99; Conservative 8; Mismatches 6;
                                      ; OTHER INFORMATION: MHC class II binding epitope US-10-468-496-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2005, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
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US-10-468-370-682
; Sequence 682, Application US/10468370
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: DETTOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: IMMUNOGENCITY
FILE OF INVENTION: IMMUNOGENCITY
FILE OF INVENTION: IMMUNOGENCITY
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT APPLICATION NUMBER: US/10/468,496
FRIOR APPLICATION NUMBER: 01103954.2
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PLING DATE: 2001-03-16
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                                                                                                                                                                             APPLICANT: Markins, John
APPLICANT: Markins, John
APPLICANT: May John
APPLICANT: May Joeffrey
APPLICANT: May Joeffrey
APPLICANT: May Joeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REPERENCE: MER-118
FILE REPERENCE: MER-118
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
SPIOR FILING DATE: 2002-04-05
SOFTWARE: FASTESO for Windows Version 4.0
SEQ ID NO 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.4%; Score 524, DB 15;
Best Local Similarity 86.7%; Pred. No. 8.2e-41;
Matches 98; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2013, Application US/10468496
Publication No. US20040180386A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                             Hamilton, Anita
Williams, Stephen
Carr, Francis J
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Jones, Tim
                                                               Carter, Graham
                                                                                                                                                         Hanlon, Marian
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APPLICANT:
APPLICANT:
APPLICANT:
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TYPE: PRT
ORGANISM: Artificial Sequence
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Carter, Graham
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                    Query Match

88.4%; Score 524; DB 16; Length 113;
Best Local Similarity 86.7%; Pred. No. 8.2e-41;
Matches 98; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.9%; Score 521; DB 15; Length 113; Best Local Similarity 85.8%; Pred. No. 1.6e-40; Matches 97; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-676
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APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Watkins, John
APPLICANT: Watkins, John
APPLICANT: Watkins, Jeffred
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REPERENCE: WER-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2002-02-18
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ 1D NOS: 689
SOPTWARE: FRANCO NOS: 689
                                                                                                                                                                                 OTHER INFORMATION: MHC class II binding epitope
                     NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2013
LENGTH: 113
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                                                                                                                                   ORGANISM: Artificial Sequence
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Williams, Stephen
Hanlon, Marian
PRIOR FILING DATE: 2001-03-20
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Jones, Tim
Carter, Graham
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LENGTH: 113
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APPLICANT:
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APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: INMUNOGENCITY
FILE REPERENCE: MER-11)
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 0110577.5
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR FILING DATE: 2001-03-15
PRIOR PLILNG DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01107012.5
PRIOR APPLICATION NUMBER: 0110699.6
PRIOR APPLICATION NUMBER: 0110699.6
PRIOR APPLICATION NUMBER: 0110699.6
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APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REFERENCE: MER-118
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87.9%; Score 521; DB 16;
Best Local Similarity 85.8%; Pred. No. 1.6e-40;
Matches 97; Conservative 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRICR APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2007
Sequence 2007, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATTON:
APPLICANT: Cart, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
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Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
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TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: INVENTION: INVENTION: MITH REDUCED
FILE REPERBACE: MER-117
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT APPLICATION NUMBER: US/10/468,496
FRIOR APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-08
PRIOR PLING DATE: 2001-03-15
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87.7%; Score 520; DB 16; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.9e-40;
Matches 97; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: De-immunized MHC class II binding epitope US-10-468-370-680
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PRIOR APPLICATION NUMBER: BP 01108291.4
PRIOR FILING DATE: 2001-04-05
PRIOR PLICATION NUMBER: PCT/EP02/01690
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 01106899.6
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2011
LENGTH: 113
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APPLICANT: Carr, Francis J.
                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
                                                                                                                                                            SEQ ID NO 680
LENGTH: 113
TYPE: PRT
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                             61 NQKFKGRVTITADKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
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APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: Way, Jeffrey
ATITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.7%; Score 514; DB 15;
Best Local Similarity 85.0%; Pred. No. 6.9e-40;
Matches 96; Conservative 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR PRIOR APPLICATION NUMBER: PCT/EP02/01690
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 678
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Job time : 70 secs
                                                                                                                                                                                          Sequence 678, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Hamilton, Anita
Williams, Stephen
                                                                                                                                                                                                                                                                                                           Carr, Francis J
                                                                                                                                                                                                                                                                                                                                                               Carter, Graham
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                                                                                                                                     RESULT 15
US-10-468-370-678
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102,

Sequence Sequence Sequence

Sequence

Sequence Sequence

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Sequence Sequence Sequence Sequence

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1 QVQLQQSGPELEKPGASVKISCKASGYSFTGYIMWWKQNNGKSLEWIGNIAPYYGGTSY
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                                                                                                                                                                                                                                                                       US-08-002-324-2
; Sequence 2, Application US/08002324
; Patent No. 5861156
; GENERAL INFORMATION:
    APPLICANT: George, Andrew J.T.
    APPLICANT: Begal, David M.
    APPLICANT: Huston, James S.
    TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO TARGET
    TITLE OF SEQUENCES: 20
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
    STREET: Two Militia Drive
    CITY: Lexington
    COUNTRY: USA
    ZIPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTITE: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,324
FILING DATE: 19930108
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/COMPUTION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECHOME: (617) 981-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
US-08-436-717-102
US-09-581-345-5
US-08-561-551-51
US-08-561-521
US-08-881-037-20
US-08-137-1170-112
US-08-436-717-112
US-08-474-040-56
US-08-477-028-56
US-08-477-028-56
US-08-477-00-56
US-08-477-00-56
US-08-477-00-56
US-08-477-00-56
US-08-477-00-56
US-08-477-00-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 473.5; DB 2; Pred. No. 2.6e-40; 13; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 981-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-002-324-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
  90;
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                                                                    Query Match
Best Local S:
Matches 90
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Sequence 57, Appl
Sequence 73, Appl
Sequence 27, Appl
Sequence 102, Appl
Sequence 102, Appl
Sequence 102, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Appl. Sequence 30, Appl. Sequence 13, Appl. Sequence 119, Appl. Sequence 119, Appl. Sequence 153, Appl. Sequence 2, Appl. Sequence 5, Appl. Sequence 5, Appl.
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8, Appli
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Sequence 2, Appli
Sequence 3, Appli
                                                                                                               (without alignments)
443.965 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                1 EVQLVQSGAEVEKPGASVKI......YYCVSGMEYWGQGTSVTVSS
                                                                                                April 18, 2005, 09:57:36 ; Search time 19 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-556-605-3

US-08-525-539A-78

US-08-525-539A-78

US-09-647-468-139

US-09-647-468-153

US-09-647-468-153

US-09-647-468-153

US-09-647-468-153

US-09-647-468-153

US-09-647-468-153

US-08-477-728-57

US-08-477-728-57

US-08-477-728-73

US-08-477-728-73

US-08-477-728-73

US-08-477-728-73

US-08-477-728-73

US-08-477-728-73

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US-08-477-728-73

US-08-477-728-73
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US-08-137-117D-102
US-08-436-717-27
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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-08-484-537-73
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                                                                                                                                                                                                                                                      513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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593
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Match 1
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                                                                      OM protein
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Gaps

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Length 130;

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2 VOLVOSGABVEKPGASVKISCKASGSSFIGYNMNWVRQNIGKSLEWIGAIDPYYGGTSYN
                                                                                                                                                                                                                                                                                            62 OKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCV----SGMEYWGQGTSVTVSS 113
                                                                                                                   Query Match
78.2%; Score 464; DB 4; Length 13
Best Local Similarity 76.7%; Pred. No. 2.6e-39;
Matches 89; Conservative 10; Mismatches 13; Indels
        ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                      1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNNWVRQNIGKSLEWIGAIDPYYGGTSY
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Sequence 3, Application US/09556605

BAPLICANT: Sallberg, Matti
APPLICANT: Sallberg, Matti
APPLICANT: Lazdina, Una
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS:
TITLE REFERENCE: TRIPEP.030

CURRENT APPLICATION NUMBER: US/09/556,605

CURRENT FILING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSEQ for windows Version 4.0

SEQ ID NO 3
                                                                                                                                                                                                            APPLICANT: 1
TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Taxington
STREET: MA
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6e-40;
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75.0%; Pred. No. 2.6e
tive 13; Mismatches
                                                                                                                                         Sequence 2, Application PC/TUS9400261
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLLING MAILS

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CBM9;
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 981-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 anino acids
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amino acid
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Best Local Similarity 75.09
Matches 90; Conservative
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                                                                                                                          PCT-US94-00261-2
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61 NQKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVYXCAVGGNYVDWFAYWGQGTLVTVSS 119
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61 QKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGKGTGFAYWGQGTLVTVSA 116
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: SCHILLBERG, Stefan
APPLICANT: SCHILLBERG, Stefan
APPLICANT: SACK, Markus
APPLICANT: MARKING, Jorg
APPLICANT: MONECKE, Michael
APPLICANT: SACK, Markus
APPLICANT: SPIEGEL, Holger
APPLICANT: EMBENAN, Sabine
APPLICANT: EMBENAN, Sabine
APPLICANT: EMBENAN, Sabine
APPLICANT: EMBENAN, Sesience
ITILE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
ITILE REFERENCE: 0147-0189P
CURRENT APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER FILING DATE: 1998-10-16
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: synthetic, OTHER INFORMATION: natural origin US-09-419-788-30
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40.08-525-539A-78
9.08-08-525-539A-78
9.08-08-08-08-78
9.08-08-08-78
9.08-08-78
9.08-08-78
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; Patent No. 6825325
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.61
Matches 90; Conservative
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Sequence 139, Application US/09647468

Patent No. 6677436

GENERAL INPORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABOTA, NAOHING
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TITLE OF INVENTION: USO9/647,468
CURRENT APPLICATION NUMBER: DS746/0289
CURRENT FILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1999-04-03
SOFTWARE: PATENTING DATE: 1998-04-03
SOFTWARE: PATENTING DATE: 2010-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NQKFKGKATLTVDKSSSTAFWHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLVQSGAEVKKPGASVKVSCKASGYSFTGYTMHWVKQSPGMNLEWIGLINPYNGGTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMWWVRQNIGKSLEWIGAIDPYYGGTSY
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US-09-647-468-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.4%; Score 453; DB 3; Length 136; 75.2%; Pred. No. 3.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
   PatentIn Release #1.0, Version #1.30
              CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-5EP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAM, TYLER
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/OFFUTION INFORMATION:
TELEPAN: (415) 813-5600
TELEPAN: (415) 8494-0792
INFORMATION FOR SED ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Mismatches
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Matches 88; Conservative
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ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-525-539A-63
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US-09-647-468-139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                   THEREOF, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THEREOF, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFQDKATLTVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
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Fatent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO,
APPLICANT: DETERSON, JERRY A.
TILLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDES
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDES
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDES
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDES
CORRESPONDENCES:
MUMBER OF SEQUENCES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
COUNTRY: USA
ZIP: 94304-1018
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOS/MS-DOS
PERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
                                 RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.4%; Score 453; DB 3; Length 117; Best Local Similarity 75.2%; Pred. No. 2.9e-38; Matches 88; Conservative 11; Mismatches 14; Indels
       TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEP NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road CITY: Pala Alto
STRATE: CA
COUNTRY: USA
ZIP: 943-41018
COMPUTER READABLE FORM: MEDION FOLDOS/MS-DOS
SOFTUM YPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE OR MEDION DATA: MEDION TYPE: 14-SEP-1995
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-600
TELEPHONE: ANDION ORNE SEQ ID NO: 78: SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPANDENDESS: single
TOWNING TOWNIN
PETERSON, JERRY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-525-539A-78
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APPLICANT:
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Gequence 140, Application US/09647468

| Gequence 140, Application US/09647468
| Patent No. 6677436
| GentsAL INFORMATION:
| APPLICANT: SATO, KOH
| APPLICANT: ADACHI, HIDEXI
| APPLICANT: ADACHI, HIDEXI
| APPLICANT: ADACHICAN UNANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND TITLE OF INVENTION: HUMANIZED ANTIBODY APPLICANTION: HUMANIZED ANTIBODY TITLE OF INVENTION: HUMANIZED ANTIBODY FILE OF INVENTION UNBER: US/09/647,468
| FILE REFERENCE: 053466/0289
| CURRENT FILING DATE: 2000-09-29
| PRIOR PILING DATE: 1999-04-02
| PRIOR FILING DATE: 1998-04-03
| PRIOR FILING DATE: 1998-04-03
| NUMBER OF SEQ ID NOS: 183
| SEQ ID NO 140
| LENGTH: 118
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| APPLICANT: SATO, KOH |
| APPLICANT: MAGNIED ANTIBODY ACAINST HUMAN TISSUE FACTOR (TF) |
| TITLE OF INVENTION: HUMANIZED ANTIBODY ACAINST HUMANIZED ANTIBODY |
| TITLE OF INVENTION: HOMBER: US/09/647,468 |
| CURRENT APPLICATION NUMBER: US/09/647,468 |
| PRIOR APPLICATION NUMBER: PCT/JP99/01768 |
| PRIOR PPLING DATE: 1999-04-02 |
| PRIOR FILING DATE: 1999-04-03 |
| NUMBER OF SEQ ID NOS: 183 |
| SOFFWARE PATENTING DATE: PATENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF OTHER INFORMATION: mouse monoclonal antibody ATR-3 US-09-647-468-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-647-468-153
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76.1%; Score 451.5; DB 4; Length 137;

Query Match

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US-U9-64/-468-154
Sequence 154, Application US/09647468
Fatent NO. 6677436
JenerA INFORMATION:
APPLICANT: SATO. KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS
CURRENT FILING DATE: 1999-04-02
PRIOR PLILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 183
SEQ ID NO 154
LENGTH: 137
LENGTH: 137
LENGTH: 137
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US-US-WED-BLAND.
US-US-WED-BLAND.
Sequence 2, Application US/09486814A
Patent No. 6562599
GENERAL INPORMATION:
APPLICANT: YANAMOTO, Hiroko
APPLICANT: HAYASHI, No. 65625910
APPLICANT: HAYASHI, No. 65625910
APPLICANT: TOHNOH, Naoki
TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
FILE REFERENCE: 0020-4682P
CURRENT APPLICATION UNMBER: US/09/486,814A
CURRENT FILING DATE: 202-06-13
NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
LENGTH: 297
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                                                                                                               20 BIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NQKFKGKATLITVDKSSSTAFWHLNSLTSEDSAVYYCARGGGGYYFDYWGQGTTLIVSS 137
                                                                                                                                                                                  61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG-----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                              1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWYRONIGKSLEWIGAIDPYYGGTSY
                                                                              1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                           5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Amino acid;
CTHER INFORMATION: sequence coding for H chain V region of ant-TF;
CTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154
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                           Indels
Best Local Similarity 72.9%; Pred. No. 5e-38;
Matches 86; Conservative 12; Mismatches 15;
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Best Local Similarity
Matches 86; Conservat
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US-09-486-814A-2
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Length 116;

DB 2;

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Query Match
Best Local Similarity
Matches 85; Conserv
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US-08-718-323A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                   1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                          40 QVKLQESGPELEKPGASVKISCKASGYSFTGYNMKWVKQSNGKSLEWIGYIYPYNGGTGY
                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS-GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Smith, Rodger
APPLICANT: Smith, Rodger
APPLICANT: Chiswell, John
APPLICANT: Chiswell, David
APPLICANT: Dataley, Michael J.
APPLICANT: Fitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Kenten, John H.
APPLICANT: Titmas, Richard C.
APPLICANT: Williams, Richard C.
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                                       Length 297;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: RADI-JULY WARE: 33,771
REGISTRATION NUMBER: 09000
                                                                                                                                                                                                                                    Query Match 75.8%; Score 449.5; DB 4; Best Local Similarity 75.4%; Pred. No. 1.9e-37; Matches 86; Conservative 12; Mismatches 15;
            ORGANISM: Mus sp., strain; Balb/c, tissue: spleen
FEATURE:
NAME/KEY: PEPTIDE
                                                                        LOCATION: (1)..(145)
OTHER INFORMATION: Identification Method:
FEATURE:
NAME/FEY: PEPTIDE
LOCATION: (177)..(279)
OTHER INFORMATION: Identification Method:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-273-146-55;
Sequence 55, Application US/08273146;
Patent NO. 5855888;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: 1GEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acida
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-273-146-55
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                                                                                                                                                                                             US-09-486-814A-2
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1 QVQLQQSGPELVKPGASVKVSCKASGYAFTNYNIYWVKQSHGKSLEMIGYIDPYSGGSSY
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                                                                                              1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                        NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG---MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVQSGAEVEXPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                   61 NQKFKGKATLITVDKSSSTAYMHLNSLTSEDSAVYYCAGGNPRFAFWGQGTTVTVS 116
                                                  Gaps
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,323A
FILING DATE: 11-No. 6204007-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09587526
Patent No. 6407214
GENERAL INFORMATION:
APPLICANT: Raymond John Owens, Martyn Kim Robinson,
TITLE OF INVENTION: Antibodies against E-selectin
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Raymond John Owens, Martyn Kim Robinson,
TITLE OF INVENTION: Antibodies against E-selectin
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                              15;

/ Score 447.5; DB 3
/ Pred. No. 1.2e-37;
11; Mismatches 18
75.5%; Score 447.5; DB 73.3%; Pred. No. 1e-37; ive 13; Mismatches ]
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3R: CARP-0054
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08718323A Patent No. 6204007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-439
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.5%;
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Best Local Similarity 76.3*
Matches 87; Conservative
                                                85; Conservative
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Pest Local Similarity 76.3%; Pred. No. 1.2e-37;
Matches 87; Conservative 11; Mismatches 15; Indels 1
                                                                                                                                            ZCOUNTRY: USA
ZIP: 191031
ZIP: 191031
ZIP: 191031
ZIP: 191031
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYZETH: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/587,526
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/718,323
FILING DATE: 11-No. 6407214-1996
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 35,719
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3109
TELEPHONE: (215) 568-3100
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APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Witholas F.
APPLICANT: SELICK, Harold B.
APPLICANT: SELICK, Harold B.
APPLICANT: SELICK, HAROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: US
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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STRANDEDNESS: si
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                                                                                 CITY: Phi
STATE: PA
COUNTRY:
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               FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIUM DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
PRIUM DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M
REGISTRATION NUMBER: 30.223
REGISTRATION NUMBER: 11823-002600
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 18, 2005, 10:07:36 Job time : 20 secs
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 73.34
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
APPLICATION NUMBER:
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